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(54) Title: GENERATION OF HUMAN CYTOMEGALOVIRUS YEAST ARTIFICIAL CHROMOSOME RECOMBINANTS

(57) Abstract: The present invention relates to a recombinant DNA construct comprising a YAC vector and at least a portion of the HCMV genome. The vector is useful as a basic research tool with which to study CMV biology, or as a vaccine with which to immunize a mammalian host against infection by CMV.

GENERATION OF HUMAN CYTOMEGALOVIRUS
YEAST ARTIFICIAL CHROMOSOME RECOMBINANTS

BACKGROUND OF THE INVENTION

5   Human cytomegalovirus (HCMV) is the leading cause of viral congenital infections

worldwide, involving about 1% of newborns. In children, the consequences may be severe,

especially in case of maternal primary infection during pregnancy. In the United States, about

30,000 to 40,000 newborns are affected each year; more than 9,000 of these children are left

with permanent neurological sequelae. Demmler, G.J., 1994, Congenital cytomegalovirus

10   infection, *Semin. Pediatr. Neurol.* 1(1):36-42. The annual cost of treating cytomegalovirus

infection complications in the United States is about two billion dollars. Daniel Y. *et al.*, 1995,

Congenital cytomegalovirus infection, *Eur. J. Obstet. Gynecol. Reprod. Biol.*, 63(1):7-16.

HCMV is a species-specific member of the herpes virus family. Other well-known

members of the herpes virus family include herpes simplex virus, types I and II, Epstein-Barr

15   virus and Varicella Zoster virus. Although these viruses are related to each other taxonomically

as double-stranded DNA viruses, infections due to these viruses manifest in a clinically distinct

manner. In the case of HCMV, medical conditions arising from congenital infection include

jaundice, respiratory distress, and convulsive seizures which may result in mental retardation,

neurologic disability or death.   As noted above, congenital HCMV infection produces

20   significant problems from both personal and public health perspectives.

Infection in adults is frequently asymptomatic, but may manifest as mononucleosis,

hepatitis, pneumonitis, or retinitis.   HCMV infection is particularly significant in

immunocompromised patients such as AIDS sufferers, chemotherapy patients, and organ

transplant patients undergoing tissue rejection therapy.

25   The mechanisms of HCMV pathogenesis are not fully understood.   It is believed that

host factors, such as cellular and/or humoral immune responses might be involved. *See*, Alford

and Britt, "The Human Herpesviruses", Eds. Roizman, B., R. J. Whitley and C. Lopez, Raven

Press, New York, 1993, pp 227-55. It has also been speculated that genetic variability (either

structural or antigenic or both) among different strains of HCMV could be responsible for the

variability in clinical manifestations observed. *See,* Pritchett, R.F., 1980, DNA nucleotide

sequence heterogeneity between the Towne and AD169 strains of cytomegalovirus, *J. Virol.*

5   36(1):152-61; Lehner, R. *et al.,* 1991, Comparative sequence analysis of human

cytomegalovirus strains, *J. Clin. Microbiol.* 29(11):2494-502; Fries, B.C., 1994, Frequency

distribution of cytomegalovirus envelope glycoprotein genotypes in bone marrow transplant

recipients, *J. Infect. Dis.* 169(4):769-74.

Classical drug therapies have generally focused upon interactions with proteins in

10   efforts to modulate their disease causing or disease potentiating functions. Such therapeutic

approaches have failed for cytomegalovirus infections.

Effective therapy for HCMV has not yet been developed despite studies on a number of

antiviral agents. Interferon, transfer factor, adenine arabinoside (Ara-A), acycloguanosine

(Acyclovir, ACV), and certain combinations of these drugs have been ineffective in controlling

15   HCMV infections. Based on preclinical and clinical data, foscarnet (PFA) and ganciclovir

(DHPG) show limited potential as antiviral agents. PFA treatment has resulted in the resolution

of HCMV retinitis in five AIDS patients to date. DHPG studies have shown efficacy against

HCMV retinitis and colitis. DHPG seems to be well tolerated by most treated individuals, but

the appearance of a reversible neutropenia, the emergence of resistant strains of HCMV upon

20   long-term administration, and the lack of efficacy against HCMV pneumonitis limit the long

term applications of this compound.

Immunoglobulin has also been utilized for treating HCMV infections. *See,* Condie,

R.M. *et al.,* 1984, Prevention of cytomegalovirus infection in bone marrow transplant recipients

by prophylaxis with an intravenous, hyperimmune cytomegalovirus globulin, *Birth Defects,*

25   20:327-344; Perrillo, R. P. *et al.,* 1987, Immune globulin and hepatitis B immune globulin,

Arch. Intern Med., 144:81-85; Snydman, D. R., *et al.* 1987, Use of cytomegalovirus immune

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globulin to prevent cytomegalovirus disease in renal-transplant recipients, *N. Engl. J. Med.*, 317:1049-1054. The development of more effective and less-toxic therapeutic compounds and methods is needed for both acute and chronic use.

Several HCMV vaccines have been developed or are in the process of development. Vaccines based on live attenuated strains of HCMV have been described. *See*, Plotkin, S.A. *et al.*, 1984, *Lancet*, 1:528-30; Plotkin, S. A. *et al.*, 1976, *J. Infect. Dis.*, 134:470-75; Glazer, J. P. *et al.*, 1979, *Ann. Intern. Med.*, 91:676-83; and U.S. Pat. No. 3,959,466. A proposed HCMV vaccine using a recombinant vaccinia virus expressing HCMV glycoprotein B has also been described. Cranage, M. P. *et al.*, 1968 *EMBO J.*, 5:3057-3063. However, vaccinia models for vaccine delivery are believed to cause local reactions. Additionally, vaccinia vaccines are considered possible causes of encephalitis.

Adenoviruses have been developed previously as efficient heterologous gene expression vectors. For example, an adenovirus vector has been employed to express herpes simplex virus glycoprotein gB (Johnson, D. C. *et al.*, 1988, *Virol.*, 164:1-14), human immunodeficiency virus type 1 envelope protein (Dewar, R. L. *et al.*, 1988, *J. Virol.*, 63:129-136), and hepatitis B surface antigen (Davis, A. R. *et al.*, 1985, *Proc. Natl. Acad. Sci., U.S.A.*, 82:7560-7564; Morin, J. E. *et al.*, 1987, *Proc. Natl. Acad. Sci., U.S.A.*, 84:4626-4630). Adenoviruses have also been found to be non-toxic as vaccine components in humans (Takajuji, E. T. *et al.*, 1970, *J. Infect. Dis.*, 140:48-53; Collis, P. B. *et al.*, 1973, *J. Inf. Dis.*, 128:74-750; and Couch, R. B. *et al.*, 1963, *Am. Rev. Respir. Dis.*, 88:394-403). U.S. Pat. Nos. 5,591,439 and 5,552,143 provide novel vaccine components for HCMV which comprise an adenovirus expression system capable of expressing a selected HCMV subunit gene *in vivo*.

Human CMV is a large, enveloped herpesvirus whose genome consists of a double-stranded DNA molecule approximately 240,000 nucleotides in length. This genome is the most complex of all DNA viruses and is approximately 50% larger than the genome of herpes simplex virus (HSV). Intact viral DNA is composed of contiguous long (L) and short (S)

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segments, each of which contains regions of unique DNA sequence flanked by homologous regions of repetitive sequence. As a group, human CMV isolates share at least 80% sequence homology, making it nearly impossible to classify cytomegaloviruses into subgroups or subtypes, although variations in the restriction endonuclease patterns of various CMV DNA preparations are identifiable in epidemiologically unrelated strains. The DNA of the prototypic strain of CMV (AD 169) has been sequenced and reported to contain a conservative estimate of 175 unique translational open reading frames (ORFs). A number of the predicted CMV gene products show homology to other human herpesvirus gene products.

The large genome of CMV is difficult to manipulate. Cloning and mutagenesis of murine CMV (MCMV) has been accomplished using a bacterial artificial chromosome ("BAC"). *See*, Messerle, *et al.* 1997, Cloning and mutagenesis of a herpesvirus genome as an infectious bacterial artificial chromosome. *Proc. Natl. Acad. Sci. U.S.A.*, **94:** 14759-14763. Cloning of MCMV in a BAC allows for manipulation of the CMV genome within the bacterial system. Another useful vector, the yeast artificial chromosome ("YAC") has been utilized to clone an infectious adenovirus (Ketner *et al.*, 1994, *Proc. Natl. Acad. Sci. U.S.A.* 91:6180-6190). However, it has not yet been demonstrated that the CMV genome could be successfully cloned into and manipulated within a yeast artificial chromosome ("YAC").

Yeast artificial chromosomes (YACs) allow the propagation of very large segments of exogenous DNA in a microbial organism that is easy to work with and grow (Schlessinger, D. 1990, Yeast artificial chromosomes: tools for mapping and analysis of complex genomes, *Trends In Genetics* 6:248-253). The great promise that YAC technology holds for studies of gene function and regulation has been strengthened by the development of methods for transferring YACs into mammalian cells and animals (Choi, T. K. *et al.*, 1993, Transgenic mice containing a human heavy chain immunoglobulin gene fragment cloned in a yeast artificial chromosome. *Nature Gen.* 4:117-123).

YAC transgenic approaches are very powerful and are greatly enhanced by the ability to efficiently manipulate the cloned DNA. A major technical advantage of yeast is the ease with which specific genome modifications can be made via DNA-mediated transformation and homologous recombination. In particular, an alternative recombinant cloning method of YAC

5   construction has recently been described (Ramsay, M. 1994, Yeast artificial chromosome cloning. *Mol. Biotech.* 1:181-201. The method involves co-transformation of a target DNA, such as the HCMV viral genome, with YAC vector arms containing appropriate DNA segments homologous to the target DNA. Recombination in the yeast cell then generates the desired YAC. A schematic of this procedure is shown in Figure 1.

10   The present invention provides a YAC vector that includes the full-length DNA sequence of the CMV virus. This vector provides a solution to the long-felt need for a CMV vaccine, and provides a tool for studying the replication of CMV using cell-line models.

SUMMARY OF THE INVENTION

The present invention provides a YAC vector that includes portions of and full-

15   length DNA sequence of the CMV virus. This vector provides a solution to the long-felt need for a CMV vaccine, and provides a tool for studying the replication of CMV using cell-line models.

The present invention provides recombinant DNA constructs and YAC vectors comprising, in certain embodiments, overlapping segments of the HCMV genome. In other

20   embodiments, the present invention provides a recombinant DNA constructs and YAC vectors comprising the entire CMV genome. This invention provides stable partial and full length YAC-HCMV clones useful for studying CMV replication, generating CMV virus and constructing CMV vaccines.

In general, the present invention provides an isolated recombinant DNA molecule

25   comprising a yeast artificial chromosome, including at least a portion of HCMV genome. In preferred embodiments the DNA molecule further comprises at least one *a* sequence.

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Preferably the HCMV genome is derived from the Towne strain or from the AD169 strain. In preferred embodiments, the recombinant DNA molecule comprises a DNA molecule selected from the group consisting of Y1-2, Y3-2, Y2-4, Y4-7 and Y5-26, described in Table 2, below. In another embodiment, the invention provides a composition suitable for use as a vaccine

5   comprising the isolated recombinant DNA molecule and a pharmaceutically acceptable excipient.

Brief Description of the Drawings

Figure 1 shows recombinant targeted cloning. A mixture of the two YAC vector arms (derived from linearized plasmids that carry targeting segments represented by black boxes) and

10   the HCMV genome (the target DNA) are simultaneously introduced into transformation competent yeast. Homologous recombination in the yeast cell amongst these DNAs results in the formation of a specific YAC clone.

Figure 2 shows plasmid maps of pRML1(AB) and pRML2(AB) derived from pRML1 and pRML2 targeting vectors.

15   Figure 3 shows an example of a pulse-field gel analysis of two yeast strains carrying different YAC-HCMV recombinants; Y5-26, lane 2; Y2-4, lane 3; and control yeast without YAC, lane 4. Left panel: the ethidium bromide-stained gel. Right panel: a Southern blot probed with STS5. The positions of the 50kb marker (lane 1) are shown, and the YAC-HCMV DNAs are marked. Note, Y5-26 co-migrates with the yeast chromosome (VI) of ~290 kb.

20   Figure 4 shows a schematic diagram of YAC-HCMV clones spanning the entire viral genome.

Figure 5 shows the transfer of Y5-26 to human foreskin fibroblast (HFF) cells, including Sequence Tagged Site (STS) analysis for the integrity of the transferred genome. M stands for the marker lane. Lane V shows viral (HCMV, Towne) injected HFF cells. Lane Y shows YAC

25   5-26 transferred cells. Lane (-) shows mock transferred cells. Representative STSs (1, 4, 5, 8, 12, 14, 16, 19, and 20) are shown.

Figure 6A shows transient transfection assays using 1 µg DNA of the plasmids described, followed by infection with HCMV at a multiplicity of infection (M.O.I.) of 10. NIH 3T3 cells were lysed at different times post infection, or at the moment of infection (mock), and the luciferase activity of the extracts was measured. The relative luciferase activity of a typical

5   experiment is shown, where triplicate measurements were taken. The relative light units (rlu) at each time post infection are normalized to the activity in the corresponding mock-infected cells. Figure 6B shows stably transfected clones that were infected with HCMV at an M.O.I. of 10; samples were taken at different times post infection. The average rlu values from at least two experiments in triplicate are shown. Clones 2A-1, 2A-3 and 2A-5 are three representative

10   clones stably transfected with pLHN.UL54wt. Clones 6A-1, 6A-2 and 6A-4 are representative clones stably transfected with pLHN.UL86.

Figure 7 shows structure of an HCMV's genome, with the Unique Long Region (UL), Unique Short Region (US), and the inverted and direct repetitive sequences. The STS panel shows the relative positions of the pairs of oligonucleotides used to check the integrity of

15   HCMV. Five YACs are shown, with their corresponding mutations outlined. The selectable markers are shown (U, *URA3*; T, *TRP1*; L, *LEU2*; P, puromycin resistance; Neo, neomycin resistance), as well as the positions of the HCMV sequences where the mutations were performed.

Figure 8A shows Pulse Field Gel Electrophoresis in which different DNA samples were

20   resolved: size markers (lane 1), YPH857 (lanes 2 and 4), Y24 (lanes 3, 5 and 6) and Y24P (lane 7). The gels were either stained with ethidium bromide (lanes 1 to 3), or hybridized to a UL54 specific probe (lanes 4 and 5, named pol) or to a puromycin specific probe (lanes 6 and 7, named puro). The sizes of the marker DNA fragments are shown in kilobases. The arrows indicate the band corresponding to either Y24 or Y24P. Figure 8B shows an agarose gel in

25   which an aliquot of the STS PCR reaction was loaded. The lanes are named V for AD169 DNA or Y for YAC DNA. The set number for the corresponding STS is indicated, as well as

the location of the size markers. Figure 8C shows PCR reactions to test the UL54-Luc and

UL86-Luc mutations, and their integration in the correct position in Y24P. Specific primers

were used, YAC54.2 and GLprimer2 (lanes 1 to 3) YAC86.2 and GLprimer2 (lanes 4 and 5).

The DNA samples are Y24P (lanes 1 and 4), Y24P/UL54wt-Luc (lane 2), Y24P/UL54IRM-Luc

5   (lane 3), and Y24P/UL86-Luc (lane 5).

Figure 9A shows Y24P/UL54wt-Luc transgenic lines were infected with HCMV at an

M.O.I. of 10. Samples were harvested at the indicated times post infection. Averages of at least

two experiments in triplicate are shown. As a negative control, Y24P/UL86-Luc clones (5C and

7E) were used. Figure 9B shows fold activation in luciferase activity in transgenic plasmid

10   pLHN.UL54wt lines (2A-1, 2A-3 and 2A-5) and Y24P/ UL54wt-Luc lines (31C, 42.8 and

44.11).

Figure 10 shows STS analysis of the YAC transgenic NIH 3T3 clones. PCR rections

were performed using specific primer sets designed along the HCMV genome. DNA from

either NIN 3T3 cells (lanes 1, 4, 7, 10, 13), yeast Y24P positive control (lanes 2, 5, 8, 11, 14) or

15   NIH 3T3/Y24P/UL54wt-luc 44.11 clone (lanes 3, 6, 9, 12, 15) was used, along with different

sets of oligos (STS), indicated in the top part of the figure.

Figure 11 shows the stable NIH 3T3 clone Y24P/UL54wt-Luc 44.11 was infected with

HCMV, at different M.O.I. from 0.005 to 10. Cells were harvested at 48 hours post-infection,

and the luciferase activity was measured. Each point represents the average of two independent

20   infections.

Figure 12 shows stable Y24P/UL54IRM-Luc NIH 3T3 clones were infected with

HCMV at a M.O.I. of 10. Samples were harvested at the indicated times and the luciferase

activity determined. Each point represents the average of at least two independent experiments

in triplicate. The fold activation was calculated dividing the absolute value by the mock-

25   infected value. Three representative clones are shown.

Figure 13 shows Y24P/UL54wt-Luc NIH 3T3 clones were infected with MCMV at a

M.O.I. of 10. Samples were harvested at the indicated times and the luciferase activity

measured. Each point represents the average of at least two independent experiments in

triplicate. The fold activation was calculated dividing the absolute value by the mock-infected

5   value. Two representative clones are shown.

Figure 14 shows the detection of HCMV IE1 and UL54 transcripts in 3T3 cells infected

with HCMV. NIH 3T3 or HFF cells were mock infected (M) or infected with HCMV at an

MOI of 1. Total RNA was harvested at different times (hour postinfection) indicated, treated

with DNase, and reverse transcribed by using oligo(dT). PCRs were performed using primer

10   sets specific for HCMV IE1 UL54, human TF (for HFF samples), and murine HPRT (for NIH

3T3 samples). Amplified products were separated on 1% agarose gels and visualized by

ethidium bromide staining. Amplified fragments obtained in the different reactions are shown.

Sizes were as expected for each primer set. Specific PCR-amplified products were not detected

in control reactions in which reverse transcriptase was not added during the RNA reverse

15   transcription reaction.

DETAILED DESCRIPTION OF THE PREFERED EMBODIMENTS

Polynucleotides of the Invention

The present invention provides a vector comprising at least a portion and up to

substantially all of a full-length CMV genome on a single nucleic acid molecule that is capable

20   of replicating in a host cell such as a yeast cell. Preferably, the CMV genome is a human CMV

(HCMV), murine CMV (MCMV), or guinea pig CMV (gpCMV) genome. In a preferred

embodiment, the CMV genome is incorporated into a yeast artificial chromosome ("YAC").

The YAC supplies *cis*-genetic elements that permit maintenance of the YAC in yeast cells

(telomeres, a centromere, and origins of replication). The YAC can also supply genetic

25   markers used to select yeast cells containing a YAC. In one embodiment, a YAC-CMV vector

is provided that incorporates portions of the pRML1 and pRML2 targeting vectors including

conditional centromere and the herpes simplex virus thymidine kinase gene under the control of

the yeast DED1 promoter and derived from pCGS966, permitting amplification of the YAC by

growth in selective medium as described previously (Spencer, F. *et al.*, 1993, Targeted

recombination-based cloning and manipulation of large DNA segments in yeast, *Methods in*

5   *Enzymology.* **5**:161-175; Hieter, P. *et al.*, 1990, Yeast artificial chromosomes: Promises kept

and pending, *Genome Analysis* **1**:83-119; Smith, D. R. *et al.*, 1990, Amplification of large

artificial chromosomes, *Proc. Natl. Acad. Sci. U.S.A.* **87**:8242-8246).

The vector may also comprise restriction enzyme sites. Digestion by the appropriate

restriction enzyme allows for liberation of virus from YAC vector DNA by restriction enzyme

10   cleavage. It is preferred that the restriction enzyme sites are absent from the CMV genome.

CMV DNA replication can be initiated by circularization of the linear virion DNA by ligation

of complementary 3' base overhangs following infection (Tamashiro, J. C. and Spector, D. H.

1986, Terminal Structure and Heterogeneity in Human Cytomegalovirus Strain AD 169. *J.*

Virol. **59**:591-604; Spaete, R. R. and Mocarski, E. S. 1985, The *a* Sequence of the

15   Cytomegalovirus Genome Functions as a Cleavage/Packaging Signal for Herpes Simplex Virus

Defective Genomes. *J. Virol.* **54**:817-824; Kemble, G. W. and Mocarski, E. S. 1989, A Host

Cell Protein Binds to a Highly Conserved Sequence Element (pac-2) within the

Cytomegalovirus a Sequence. *J. Virol.* **63**:4715-4728; McVoy, M. A. and Adler, S. P. 1994,

Human Cytomegalovirus DNA Replicates after Early Circularization by Concatamer

20   Formation, and Inversion Occurs within the Concatemer. *J. Virol.* **68**:1040-1051). In a

preferred embodiment, the pRML vectors comprise a *Pac* I site at one end of the YAC-encoded

virus (**Fig. 2**).

The targeting segments for cloning CMV virion DNA may be derived either from

natural restriction products or PCR products. The CMV DNA can comprise at least a portion of

25   a CMV genome. Preferably, the CMV comprises about at least 50, 100, 500, 1,000, 5,000,

10,000, 100,000, 150,000, or 200,000 base pairs of CMV DNA. Preferably, the CMV DNA

comprises an entire CMV genome. It has been shown that infectious virion DNA contains a variable number (at least two) of *a* sequence copies at the long-arm terminus and a single or no *a* sequence at the short-arm terminus (Tamashiro, J. C. and Spector, D. H. 1986, *J. Virol.* 59:591-604; Spaete, R. R. and Mocarski, E. S. 1985, *J. Virol.* 54:817-824; Kemble, G. W. and Mocarski, E. S. 1989, *J. Virol.* 63:4715-4728; McVoy, M. A. and Adler, S. P. 1994, *J. Virol.* 68:1040-1051). In the instant invention, the targeting vectors for the long-arm terminus preferably comprise an *a-a* fragment while the short arm terminus fragment preferably contains a single *a* sequence immediately flanked by a restriction enzyme site, preferably that of *Pac*I.

An *a* sequence for use in the instant invention may be obtained by cloning the genomic termini of CMV such as that of the Towne CMV strain. It is possible to utilize *a* sequences obtained from other CMV strains, although the Towne strain is a preferred source. CMV DNA may be isolated from purified virions and blunt ended using T4 DNA polymerase. The DNA may then be cut with *Xma*I restriction endonuclease and ligated to the pBS-Sk (Stratagene) vector digested by *Xma*I and *Hinc*II. The resultant library of ligated fragments are then subjected to PCR using a nested set of primers. The products of the final PCR step are directly cloned into a vector such as pGEM-T (Promega).

To construct CMV YACs, target DNA is isolated from purified virions. The linearized targeting YAC vector clones may then be introduced, along with CMV virion DNA, into yeast spheroplasts. After transformation, transformants are selected, colony purified, and examined to identify YAC-containing cells. Transformants may be analyzed by, for example, polymerase chain reaction (PCR) using a battery of Sequence-Tagged Sites (STSs). An STS is typically defined by those skilled in the art as a short tract of DNA that can be specifically detected by a corresponding PCR assay and are used as the landmarks on which to base the physical maps of the YAC clones (Nemani, M. *et al.*, 1994, A YAC Contig in 6p23 Based on Sequence Tagged Sites. *Genomics* 22:388-396). STS screening has been found to be a rapid method for identifying candidate YAC clones because direct colony PCR assays can be performed. Clones

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demonstrating the correct STS-content are then examined by pulsed-field gel electrophoresis and Southern blot hybridization to confirm the presence of a YAC of the expected size carrying CMV virion DNA.

Full length YAC-CMV clones are transferred to a permissive mammalian cell line or
5   fresh tissue sample following isolation and fractionation of yeast chromosomal DNA by, for example, pulsed-field electrophoresis.   A preferred permissive cell is a human foreskin fibroblast.   Other preferred permissive cell lines include human glioblastoma, U373 MG (available from American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209 as ATCC No. HTB-17); human embryonic lung fibroblast, HEL
10   299 (available as ATCC No. CCL-137), and human glioblastoma, U-138 MG (available as ATCC No. HTB-16).

CMV-YAC DNA can be isolated and fractioned by extracting the DNA from agarose gels using GELase-based procedures to avoid shearing of the DNA.   CMV virions can be embedded in agarose plugs and the viral membranes and proteins removed.   The plugs
15   containing virion DNA can be inserted into loading wells for separation by PFGE. Following PFGE, virion DNA bands can be located by size and extracted by, for example, GELase digestion (Epicenter, Inc).   A second separation by PFGE can be done to detect any DNA degradation. Following extraction of HCMV-YAC DNA, the DNA can be introduced into the permissive cells by any of several well-known techniques for transfecting cells, including but
20   not limited to calcium phosphate precipitation, direct micro-injection, liposome-mediated transfection, or spheroplast fusion, for example.   Such methodologies are described in *YAC Protocols* (1996), Methods in Molecular Biology, (The Humana Press Inc., Clifton, NJ).

The vectors described herein are also useful for studying the function of essential *cis* acting genes or nucleic acid sequences. For example, the vectors may be utilized to study the
25   regulation of genes essential to viral replication, the function of the origin of replication, to

generate multiple mutations in a single large DNA molecule, or generate cell-based reporter

systems for monitoring the infectious program of a virus.

A major advantage of the vectors described herein is the ease and rapidity with which

single or multiple mutations may be introduced into a CMV DNA sequence. The capacity of

5   the vectors described herein to generate multiple mutations exceed the capacity of other vectors

such as the bacterial artificial chromosome (BAC).

Compositions Comprising YAC-CMV Polynucleotides

The invention also provides compositions comprising YAC-CMV polynucleotides.

Compositions of the invention preferably comprise a pharmaceutically acceptable carrier. The

10   carrier should not itself induce the production of antibodies harmful to the host.

Pharmaceutically acceptable carriers are well known to those in the art. Such carriers include,

but are not limited to, large, slowly metabolized, macromolecules, such as proteins,

polysaccharides such as latex functionalized sepharose, agarose, cellulose, cellulose beads and

the like, polylactic acids, polyglycolic acids, polymeric amino acids such as polyglutamic acid,

15   polylysine, and the like, animo acid copolymers, peptoids, lipitoids, and inactive virus particles.

Pharmaceutically acceptable salts can also be used in compositions of the invention, for

example, mineral salts such as hydrochlorides, hydrobromides, phosphates, or sulfates, as well

as salts of organic acids such as acetates, proprionates, malonates, or benzoates. Especially

useful protein substrates are serum albumins, keyhole limpet hemocyanin, immunoglobulin

20   molecules, thyroglobulin, ovalbumin, tetanus toxoid, and other proteins well known to those of

skill in the art. Compositions of the invention can also contain liquids or excipients, such as

water, saline, glycerol, dextrose, malodextrin, ethanol, or the like, singly or in combination, as

well as substances such as wetting agents, emulsifying agents, or pH buffering agents.

Liposomes can also be used as a carrier for a composition of the invention.

25   If desired, co-stimulatory molecules, which improve immunogen presentation to

lymphocytes, such as B7-1 or B7-2, or cytokines such as MIP1α, GM-CSF, IL-2, and IL-12,

can be included in a composition of the invention. Optionally, adjuvants can also be included

in a composition. Adjuvants which can be used include, but are not limited to MF59-0,

aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP),

N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637), referred to as nor-MDP),

5   N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn

-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and

RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A,

trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80

emulsionOptionally, the efficiency of delivery of E1E2 or E2 polynucleotides may be improved

10   by injection of cardiotoxin, purified from the venom of *Naja nigricollis,* about one week prior

to an E1E2 or E2 polynucleotide injection. A muscle is injected with from about 0.1 to 20 μM

of cardiotoxin dissolved in a pharmacologically acceptable vehicle, such as 0.9% NaCl.

Methods of Eliciting an Immune Response

15   This invention also relates to methods of eliciting an immune response and/or protective

immunity in a vertebrate by introducing into the vertebrate a DNA vaccine which comprises a

YAC comprising DNA encoding an antigen or antigens, *e.g.,* capsid proteins or polypeptides, of

CMV. The uptake of the DNA vaccine by a host vertebrate results in the expression of

structural and non-structural proteins, thereby eliciting humoral or cell-mediated immune

20   responses, or both, which can provide protection against infection and/or prevent clinically

significant cytomegalovirus-caused disease. A CMV deletion mutant may also be synthesized

and incorporated into the CMV-YAC construct as a vaccine. One may also utilize a CMV-

YAC vector carrying an attenuated or non-replicative CMV genome for direct injection into

animal tissue as a vaccine.

25   YAC-CMV constructs of the invention can be used to elicit an immune response in a

vertebrate. Elicitation of an immune response can be used, *inter alia,* to provide model systems

to optimize immune responses to CMV and to provide prophylactic or therapeutic-treatment against CMV infection. YAC-CMV constructs can be used to produce CMV-specific polyclonal and monoclonal antibodies. HCV-specific polyclonal and monoclonal antibodies specifically bind to CMV antigens or epitopes. Preferably, HCMV epitopes are found within

5   the envelope glycoprotein B (gB), for example, the AD-1 epitope (codons 552-635), or the amino terminal 513 amino acids of gB. Preferably, HCMV epitopes are found in the Immediate Early protein (IE), such as the 1E1 epitope. Additional HCMV epitopes are described in Lindenmaier et al., *Arch. Virol.* 113:1-16 (1990). CMV-specific T cells activated by CMV proteins preferably recognize an epitope of a CMV polypeptide. CMV-specific T cells can be

10   $CD8^+$ or $CD4^+$.

Detection and/or quantification of an immune response, such as antibody titer, after delivery of construct of the invention can be used to identify CMV epitopes that are particularly effective at eliciting a CMV immune response. Antibodies elicited by a particular CMV epitope can then be tested using, for example, an ELISA assay to determine which polypeptides

15   contain epitopes that are most effective at generating a strong response. CMV polypeptides or fusion proteins which contain these epitopes or polynucleotides encoding the epitopes can then be constructed and used to elicit a strong CMV immune response.

A YAC-CMV construct of the invention can be administered to a vertebrate, such as a fish, bird, mouse, rabbit, guinea pig, piglet, macaque, baboon, chimpanzee, or human, to elicit

20   an immune response *in vivo*. Injection of a YAC-CMV construct is preferred. Injection of a construct results in the synthesis of a CMV polypeptide or polypeptides in the host. Thus, the CMV polypeptide is presented to the host immune system with native post-translational modifications, structure, and conformation. A YAC-CMV construct is preferably delivered as "naked DNA." Administration of a YAC-CMV construct can be by any means known in the

25   art, including intramuscular, intradermal, intraperitoneal, or subcutaneous injection, including injection using a biological ballistic gun ("gene gun"). Administration may also be intranasal

or oral. Preferably, a YAC-CMV construct is accompanied by a protein carrier for oral administration. A combination of administration methods may also be used to elicit a CMV immune response.

Administration of a YAC-CMV construct can elicit an anti-CMV immune response in the vertebrate that lasts for at least 1 week, 2 weeks, 1 month, 2 months, 3 months, 4 months, 6 months, 1 year, or longer. Optionally, an anti-CMV immune response can be prolonged by providing one or more booster injections of the construct at 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 1 year, or more after the primary injection.

A composition of the invention comprising a YAC-CMV construct is administered in a manner compatible with the particular composition used and in an amount which is effective to elicit an anti-CMV immune response, as detected by, for example, an ELISA. A YAC-CMV construct is preferably injected intramuscularly to a large mammal, such as a baboon, chimpanzee, or human, at a dose of 1 ng/kg, 10 ng/kg, 100 ng/kg, 1000 ng/kg, 0.001 mg/kg, 0.1 mg/kg, or 0.5 mg/kg. A YAC-CMV construct can be administered either to a vertebrate that is not infected with an CMV or can be administered to an CMV-infected vertebrate. The particular dosages of YAC-CMV constructs in a composition will depend on many factors including, but not limited to the species, age, and general condition of the vertebrate to which the composition is administered, and the mode of administration of the composition. An effective amount of the composition of the invention can be readily determined using only routine experimentation. *In vitro* and *in vivo* models can be employed to identify appropriate doses. If desired, co-stimulatory molecules or adjuvants can also be provided before, after, or together with the YAC-CMV compositions.

Immune responses of the vertebrate generated by the delivery of a composition of the invention, can be enhanced by varying the dosage, route of administration, or boosting regimens. Compositions of the invention may be given in a single dose schedule, or preferably in a multiple dose schedule in which a primary course of vaccination includes 1-10 separate

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doses, followed by other doses given at subsequent time intervals required to maintain and/or

reinforce an immune response, for example, at 1-3 months for a second dose, and optionally at

3-6 months for a third dose, and if needed, a subsequent dose or doses after several months.

In accordance with another aspect of the present invention there are provided isolated

5   recombinant DNA molecules contained in ATCC Deposit No. PTA-2186 and ATCC Deposit

No. PTA-2187 deposited with the American Type Culture Collection, 10801 University

Boulevard, Manassas, Va. 20110-2209, USA, on July 3, 2000. The deposited materials are

yeast cell strains that contain, respectively, the y5-26 and y2-4 recombinant DNA molecules.

The deposits have been made under the terms of the Budapest Treaty on the International

10   Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. The strain

will be irrevocably and without restriction or condition released to the public upon the issuance

of a patent.

These deposits are provided merely as convenience to those of skill in the art and are not

an admission that a deposit is required under 35 U.S.C.§112. The present invention is not to be

15   limited in scope by the constructs deposited, since the deposited embodiment is intended as a

single illustration of one aspect of the invention and any constructs that are functionally

equivalent are within the scope of this invention. The deposit of material herein does not

constitute an admission that the written description herein contained is inadequate to enable the

practice of any aspect of the invention, including the best mode thereof, nor is it to be construed

20   as limiting the scope of the claims to the specific illustration that it represents.

The sequence of the polynucleotides contained in the deposited materials, as well as the

amino acid sequence of the polypeptides encoded thereby, are controlling in the event of any

conflict with any description of sequences herein. A license may be required to make, use or

sell the deposited materials, and no such license is hereby granted. References to

25   "polynucleotides," "clones," "YAC" and 'yeast artificial chromosome" throughout this

specification includes the DNA of the deposit referred to above.

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Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook *et al.*, 1989, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY); *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991,

5   Academic Press, San Diego, CA); *PCR Protocols: A Guide to Methods and Applications* (Innis *et al.*, 1990, Academic Press, San Diego, CA); *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney, 1987, Liss, Inc. New York, NY); *Methods in Molecular Biology (Vol. 7), Gene Transfer and Expression Protocols*, (Ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.); Ramsay, M., 1994, Yeast artificial cloning, *Molec. Biotech.* 1:181-

10   201; Smith, *et al.*, 1990, Amplification of large artificial chromosomes, *Proc. Natl. Acad. Sci. U.S.A.* 87: 8242-8246; and, *YAC Protocols, Methods in Molecular Biology*, (Markie, D., 1996, The Humana Press, Inc., Clifton, NJ).

The following are provided for exemplification purposes only and are not intended to limit the scope of the invention described in broad terms above. All references cited in this

15   disclosure are incorporated herein by reference.

EXAMPLES

Example 1

Generation of a HCMV-YAC Vector

pRML vectors were engineered (**Fig. 2**) to possess a *Pac* I site at the end of the YAC-
encoded virus to allow liberation of virus from YAC vector DNA by restriction enzyme
cleavage. *Pac* I cleavage sites are not present within the HCMV genome and produce the
appropriate overhang for recircularization of the genome after transfection of permissive host
cells. The pRML vectors form the backbone of the linearized targeting YAC vector clones.

The targeting segments for cloning CMV virion DNA were derived either from natural
restriction products or PCR products. To ensure the production of infectious DNA, the correct
structure of the termini was maintained. The targeting vectors for the long-arm terminus were
designed to include an *a-a* fragment while the short arm terminus fragment contains a single *a*
sequence immediately flanked by a *Pac*I site.

The *a* sequence used in the construction of the targeting vectors was obtained by cloning
the genomic termini of HCMV Towne virion DNA. HCMV Towne DNA isolated from
purified virions was blunt ended using T4 DNA polymerase, subsequently cut with *Xma*I
restriction endonuclease and ligated to the pBS-SK (Stratagene) vector resected by *Xma*I and
*Hinc*II. This library of ligated fragments was then subjected to PCR using a nested set of
primers. The outside primer set used the M13 primer and an HH4 primer, 5'-
ACGTCGCTTTTATTCGCCGTCG (SEQ ID NO:1) designating a terminal sequence (position
109 to 130). The inside primer set used the T7 primer and HH3 primer 5'-
ACACACGCAACTCCAAGTTTCAC (SEQ ID NO:2) (position 51 to 73). The products of the
final PCR step were directly cloned into the pGEM-T vector (Promega). An analysis of these
clones confirms characterizations of the ends of the HCMV genome (Tamashiro, J. C. and
Spector, D. H. 1986. Terminal structure and heterogeneity in human cytomegalovirus strain
AD169, *J. Virol.* **59**(3): 591-604).

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The target DNA was prepared from purified virions. The linearized targeting YAC

vector clones were then introduced, along with HCMV virion DNA, into yeast spheroplasts.

After transformation, TRP1 URA3 transformants were selected, colony purified, and examined

to identify YAC-containing cells. Transformants were first analyzed by polymerase chain

5   reaction (PCR) using a battery of Sequence-Tagged Sites (STSs). An STS is defined as a short

tract of DNA that can be specifically detected by a corresponding PCR assay and are used as

the landmarks on which to base the physical maps of the YAC clones (Nemani, M., *et al.*, 1994.

A YAC Contig in 6p23 Based on Sequence Tagged Sites. *Genomics* 22:388-396). STS

screening has been found to be a rapid method for identifying candidate YAC clones as direct

10   colony PCR assays can be performed. The STS markers utilized in generating the vectors of

the present invention are illustrated in **Table 1**. Each STS produces a specific size fragment

containing a diagnostic restriction enzyme cleavage site.

Table 1

HCMV STS markers developed for mapping HCMV-YAC vectors

SETS	LOCUS	LEFT PRIMER (SEQ ID NO:)	RIGHT PRIMER (SEQ ID NO:)	SIZE	TEST CUT	SIZES (bp)
Set 22	3807-4186	ATCAGGATCGGCGACAG (3)	CGTTATCCGTTCCTCG (4)	379	EcoR I	160, 219
Set 1	11157-11706	ACGAGGTAATCAACGT (5)	ATGTTAAGCCTTAGTC (6)	549	EcoR I	407, 142
Set 2	16978-17400	GACACCTCTATGTTAC (7)	CGTATATGTACGTCAT (8)	423 (?)	Hind III	266, 157
Set 3	25799-26218	TAGACAGTATACCCTC (9)	AGTACCACATTTTGC (10)	419	EcoR I	295, 124
Set 4	36489-36714	ACATGGATTCGTGCAC (11)	ATCGATCTGGAGCACT (12)	225	EcoR I	184, 41
Set 5	53844-54093	GTGAAGCCGATACGAG (13)	AGGAGACCACGGTTTG (14)	249	EcoR I	79, 170
Set 6	66701-67183	GGTCCGCAACTTCTGATCCA (15)	CAGATCAGTCCACAGGTTCT (16)	482	Bam HI	233, 249
Set 7	73910-74261	GCTACCTTGTGCAGTC (17)	GTCCTACGTTGCTACT (18)	351	EcoR I	207, 144
Set 8	84721-85094	ACGCAGGTGAATATCC (19)	AGGTTATCGTCAAGCG (20)	373	Hind III	143, 230
Set 9	107480-107920	CACCATCTTAGGGACGACGTCTC (21)	GCATGCTCAAGACACATGCTGA (22)	440	Hind III	197, 243
Set 10	128975-129337	GATGGTGGAAATCGGA (23)	ACCTGTCGGTTGAAGC (24)	362	Hind III	193, 169
Set 11	136625-136969	TCGTCGACGCATCTGT (25)	ATATCGCACCGATTGC (26)	344	Hind III	80, 264
Set 12	149371-149770	GTTGGGCGTTGAGCACGTCTA (27)	AGCCGACAACCTGCTGCACT (28)	399	Hind III	274, 125
Set 13	155668-156028	TAAGTGGAAGTGGCCG (29)	GACGACGATGACCTCA (30)	360 (?)	Hind III	195, 155
Set 14	163686-164040	CAGCAATGTTAGCGAG (31)	TCACGCGACTGTCATA (32)	354	EcoR I	149, 205
Set 15	175465-175737	GTGAAGCGGATTGCACA (33)	TCAGGTGCGATTGACG (34)	272	EcoR I	59, 213
Set 16	185281-185620	CGTTATCCGTTCCTCG (35)	CTTGCGGAATTGACAT (36)	339	EcoR I	214, 125
Set 17	195675-196056	TATCGTTCGGACGGGA (37)	TTGGATCAGACTCACG (38)	381	Hind III	162, 219
Set 18	206161-206390	AATCACCGTCATTCCC (39)	CTCCTCAGCTTGTTGT (40)	229	Hind III	64, 165
Set 19	213192-213496	CTAGCACGATAAGGCG (41)	TGACATGTGGCGTACA (42)	304	EcoR I	244, 60
Set 20	221934-222268	AGTTGGACTACGAAGA (43)	CTGTATGTAGAAGACG (44)	334	EcoR I	123, 211
Set 21	226671-227018	TCCATAACCACCGTGG (45)	GCTGTCGCCACTTTCTG (46)	347	Not I	224, 123

Those clones that were positive for the correct STS-content (listed in Table 2, below)

were then examined by pulsed-field gel electrophoresis and Southern blot hybridization to

confirm the presence of a YAC of the expected size carrying HCMV virion DNA.

Table 2

SUMMARY OF HCMV STS-POSITIVE CLONES

CLONE	PLASMID 5'	PLASMID 3'	SEQUENCE (Ref: GenBank No: X17403) (SEQ ID NO:64)
Y 1-2	pRML1 (H+)	pRML2 (ura)+Ea	119901-178816
Y 3-2	pRML1 (+V)	pRML2 (ura)+Ea	88024-178816
Y 2-4	pRML1 (I2)	pRML2 (ura)+Ea	1-178816(*)
Y 4-7	pRML1 (+d)	pRML2 (ura)+Enx	162053-222057
Y 5-26	pRML1 (I2)	pRML2 (ura)+Enx	1-222057(*)

(*) The insert in plasmid pRML1(I2) goes from nucleotide 228426 (*Not*I) to the 3' end of the genome (nucleotide 229075), conjoined to nucleotides 1 through 3967 of the 5' end of the genome.

Example 2

Infectious HCMV DNA

HCMV DNA was transferred to permissive human foreskin fibroblasts by first isolating

5   and fractionating chromosomal DNA by pulsed-field electrophoresis. In general, HCMV-YAC

DNA was extracted from agarose gels using GELase-based procedures to avoid shearing of the

DNA. HCMV virions were embedded in agarose plugs, viral membranes and proteins were

removed, and then the plugs containing virion DNA were inserted into loading wells for

separation by PFGE. Following PFGE, virion DNA bands were located by size (~240 kb) and

10   extracted by GELase digestion as indicated by the manufacturer (Epicenter, Inc.). Free DNA

recovered by GELase digestion did not undergo any observable change in band mobility during

a second separation by PFGE, indicating that the GELase procedure did not cause any

detectable DNA degradation. To avoid shear-induced degradation of the DNA as much as

possible, the GELase enzyme was not removed following digestion.

15   In general, an aliquot of the GELase-purified HCMV DNA was introduced into

mammalian cells by either calcium phosphate precipitation methods or by direct micro-

injection. Preferably, standard methodologies or modifications thereof for calcium phosphate

precipitation methods were used.

In general, transfections were performed by the calcium phosphate precipitation method

20   using standard protocols with a slight modification. Yeast DNA (in 1 ml) was mixed with 100

μl of 2.5 M $CaCl_2$ in 1 ml of BSE 1X, incubated for 10 minutes at room temperature and added

to the cell cultures seeded in 100 mm dishes containing 20 ml of medium.

Preferably, the mammalian cells used were human foreskin fibroblast (HFF) cells. After

three weeks of incubation, the HFF cells were harvested and examined for infectious virus. In

25   three independent experiments, infectious particles were recovered at a level of ~1-10 X 10^5

FFU/ug of virion DNA. Thus, recovery of infectious virus has been demonstrated for full length HCMV DNA following PFGE.

Example 3

5   *Full-length HCMV-YAC Clones*

The full-length recombinant clone Y5-26 was isolated and shown to be replication-competent in HFF cells. Fourteen independent transfers were performed, of which 50% of the cells in four of the cultures developed cytopathic effects (CPE) between days 30 to 40 post-transfer.

10   Cultures were harvested on day 45 post transfer. All of the CPE positive cultures, but not the CPE negative cultures, tested positive for the presence of viral DNA. One of these cultures showed extremely high levels of viral DNA, comparable to a fully permissive infection with wild-type virus. The high expressor appears to have an intact genome based on an STS analysis, suggesting that Y5-26 DNA is replication competent.

15

Example 4

The HCMV-YAC Vector as a Tool for Basic Research: Demonstration of virus over host factors in cross-species activation of HCMV early gene expression

CMV is a pathogen with a highly restricted spectrum of hosts, and HCMV has a very

20   strong species specificity. HCMV can only replicate in human cells. In other species cells, HCMV can efficiently enter cells, indicating that the species restriction is not at the level of viral binding or penetration. Nowlin *et al., J. Virol.* 65:3114-21 (1991). Recent studies have provided direct evidence to show that major IE expression determined by viral immediate-early regulatory sequences is also not species restricted. Angulo *et al. J.Virol.* 72:8502-9 (1998);

25   Grzimek *et al. J. Virol.* 73:5043-55 (1999).

24

This Example demonstrates that an essential early gene activation pathway governed by HCMV major IE proteins is conserved between host species. However, a marked divergence in the mechanism for this activation between viral species is observed.

Plasmid based analysis of HCMV UL54 promoter activity in NIH 3T3 cells, using

5   **transient expression assays and stable cell lines.**

The activation of the HCMV UL54 promoter by HCMV in murine cells using a plasmid based transient expression assay was investigated. For these experiments, a 445 bp DNA fragment containing the UL54 promoter (nucleotide positions 80996 through 81441, numbered with respect to SEQ ID NO:64) was cloned in the plasmid pLHN, to produce pLHN.UL54wt.

10   A 432 bp DNA fragment, corresponding to the UL86 promoter (nucleotide positions 128318 through 128750, numbered with respect to SEQ ID NO:64) was cloned into pLHN, deriving pLHN.UL86.

Briefly, yeast strain YPH857 (Matα *ura3-52 lys2-801 ade2-101 his3Δ200 trp1Δ63 leu2Δ1 cyh2^R*) and derivates were grown in standard media. See Guthrie, C. and G.R. Fink.

15   1991, Guide to yeast genetics and molecular biology. Methods Enzymol. 194:1-863. Murine NIH 3T3 fibroblasts (ATCC CRL 1658) were propagated in Dulbecco's modified essential medium supplemented with 2 mM glutamine, 100 U penicillin per ml, 100 μg gentamicin per ml, and 10% calf serum. The AD169 and Towne strains of HCMV (ATCC VR-538 and VR-977 respectively) and the Smith strain of MCMV (ATCC VR-1399) were used.

20   pRML1 and pRML2 were used to create a series of right and left arm plasmids of the YACs, respectively. See Spencer, C. Connelly and P. Hieter. 1993, Targeted recombination-based cloning and manipulation of large DNA segments in yeast. *Methods* 5:161-175. pRML1+I₂, the right arm plasmid, was constructed in three steps: first, an *EcoR* I fragment from the cosmid pCM1035 (Pari, G.S. and D.G. Anders. 1993, Eleven loci encoding trans-

25   acting factors are required for transient complementation of human cytomegalovirus oriLyt-

dependent DNA replication. *J. Virol.* 67:6979-88) containing the last 7297 bp of the 3' end of

HCMV, plus the 3967 first bp of the 5' end, was cloned into pBluescript-SK (Stratagene, US),

deriving pBS-SK-I$_1$. This plasmid was digested with *Not* I and self-ligated, creating pBS-SK+I

and I$_2$. The fragment *Not* I-*Cla* I from pBS-SK+I$_2$ was purified and ligated to pRML1

5   (Spencer, C. Connelly and P. Hieter. (1993), supra) to construct pRML1+I$_2$. This plasmid has

4895 bp of the 5' end of HCMV. pRML2(ura)+Ea, the left arm plasmid, was constructed by

cloning a 3292 bp *EcoR* I fragment (175524 to 178816) (SEQ ID NO:64) from the cosmid

pCM1050 into pRML2 (Pari, G.S. and D.G. Anders. (1993), supra; Spencer, C. Connelly and P.

Hieter. (1993), supra). YPH857 has the appropriate auxotrophies to select for both YAC arm

10   plasmids. For the construction of pRML2-Leu2-PUR the *Pvu* II-*BamH* I 1.4 kb DNA fragment

from pPUR was inserted into the blunt-ended *BamH* I of pRML2-LEU2 (LEU2 is a yeast

protein involved in the synthesis of leucine, which complements the *leu2* mutation of YPH857),

to produce pRML2/D. Then, the LEU2 yeast gene was cloned in the place of URA3, as a *Hind*

III DNA fragment. In order to develop a mutagenesis shuttle plasmid, in which to clone the

15   different promoters, we generated pLHN. This plasmid has the yeast *HIS3* gene as a selectable

marker in yeast, the neomycin resistance gene for selection in mammalian cells, and the

luciferase gene as a reporter. The promoter sequence and the 3' end of the targeted gene are

both cloned, flanking the unique *Sma* I restriction site. pLHN.UL54wt was constructed as

follows: a 445 bp DNA fragment from the UL54 promoter (nucleotide positions 80996 through

20   81441 of HCMV genome, Genbank accession number X17403 (SEQ ID NO:64)), present in

the plasmid pPolCAT (Stenberg, R.M. *et al.* 1990, Promoter-specific trans activation and

repression by human cytomegalovirus immediate-early proteins involves common and unique

protein domains. *J. Virol.* 64:1556-65), along with an additional viral DNA fragment from the

3' region of UL54 (nucleotide positions 77291 through 77516), were cloned into the

25   multicloning site of pLHN, leaving a unique *Sma* I site in between them. Digestion with *Sma* I

directs the recombination to the UL54 locus.

pLHN.UL54IRM was constructed by cloning the mutated *EcoR* I-*Sma* I DNA fragment, into *EcoR* I-*Sma* I digested pLHN.UL54wt, replacing the wt fragment with the mutant one. IRM mutagenesis was used for this step. Briefly, the mutagenesis of the inverted repeat IR1 in the UL54 promoter was done as previously described. See Kerry, J.A. *et al.* 1996, Multiple regulatory events influence human cytomegalovirus DNA polymerase (UL54) expression during viral infection. *J. Virol.* 70:373-82. The QuickChange site-directed mutagenesis kit (Stratagene, USA) was used, following the instructions of the manufacturer. Briefly, 50 ng of pLHN.UL54wt DNA was mixed with the oligos IRM-A (GACACGTCGTTACAGATATCGCCTTC CTACGAGG) (SEQ ID NO:47) and IRM-B (CCTCGTAGGAAGGCGATATCTGTA ACGACGTGTC) (SEQ ID NO:48), 125 ng each, and then incubated for 1 minute at 95°C, followed by 16 PCR cycles (30 seconds at 95°C, 1 minute 55°C, 15 minutes 68°C). The reactions were digested with *Dpn* I, and the digested DNA was transformed into *E. coli*. Several clones were analyzed with *EcoRV*, a unique restriction site introduced with the IRM mutation. Positive clones of the new pLHN.UL54IRM plasmid were confirmed by sequencing.

PCR was used to test the correct integration of pLHN.UL54wt into the viral sequences of Y24P. Two oligonucleotides were used, YAC54.2 (TCGCCCTGGATATCGACCCGCT) (SEQ ID NO:49), complementary to a region of the UL54 promoter outside of the one included in the plasmid pLHN.UL54wt, and GLprimer2 (CTTTATGTTTTTGGCGTCTTCCA)(SEQ ID NO:50), complementary to the 5' region of the luciferase gene.

pLHN.UL86 was constructed as follows: a 432 bp DNA fragment, encompassing the UL86 promoter (nucleotide positions 128318 through 128750 of HCMV genome (SEQ ID NO:64), was cloned along with a 522 bp DNA fragment from the 3' end fragment of the UL86 gene (nucleotide positions 124981 through 125503), with a *Sma* I site in between them (Figure 6A). PCR was used to test the correct integration of pLHN.UL86 into the viral sequences of

Y24P. Two oligonucleotides were used, YAC86.2 (GTAGCCGGAGACGGCGGTT) (SEQ ID

NO:51), complementary to a region of the UL86 outside of the one included in the plasmid

pLHN.UL86, and GLprimer2 (SEQ ID NO:50).

5   In these recombinants the UL54 and UL86 promoters drive the expression of the

luciferase reporter gene. To test if the species restriction for HCMV in murine cells occurs at

early times, each plasmid was transiently transfected into NIH 3T3 cells, which were then

infected with HCMV, and luciferase activity measured at different times post infection.

           Briefly, NIH 3T3 cells were grown in Dulbecco's modified Eagle's medium,

supplemented with 10% calf serum. Transfections were done in 6-well plates, unless otherwise

10   noted, using the calcium phosphate precipitation method. See Galang, C.K., C.J. Der, and C.A.

Hauser. 1994, Oncogenic Ras can induce transcriptional activation through a variety of

promoter elements, including tandem c-Ets-2 binding sites. *Oncogene* 9:2913-21. For transient

transfections, cells were washed with PBS 16-18 hours after the addition of the precipitate, then

incubated 24 hours with 10% calf serum supplemented medium and finally infected with either

15   the Towne strain of HCMV or the Smith strain of MCMV, in 3% calf serum. Stable

transfections were done the same way, except that after the 24 hours recovery in 10% calf

serum medium, cells were selected on 400 μg/ml G418 (GIBCO BRL, USA). Clones appeared

10 days after selection. Virus was adsorbed for 2 hours prior to the addition of fresh overlay

medium.

20   To measure the luciferase activity, the Luciferase Assay System (Promega) was used,

following the directions recommended by the manufacturer. Cells were washed twice with

PBS, and 200 μl Lysis Buffer (provided by the manufacturer) were added to each well. Cells

were scraped and transferred to an Eppendorf tube, frozen and thawed and centrifuged for 2

minutes. The luciferase assays were done in a Micro plate Luminometer LB 96V (EG&G

25   Berthold), using 100 μl extract and injecting 100 μl of Luciferase Substrate, using 2 seconds

delay and 20 seconds reading time. The luciferase activity is shown either as the absolute value in relative light units (rlu), as an average of at least two experiments done in triplicate, or as fold activation, in which the absolute value is divided by the corresponding mock-infected sample.

5   As shown in Figure 6A, the infection caused a general activation of transcription, reflected by a 5-fold activation of the promoter-less pGL3-basic plasmid 24 hours post infection when compared to the mock infected sample, followed by a 2.5-fold activation at 48 hours post infection. The overall activation of UL54 promoter was slightly higher (6-fold), but the fold activation was at a similar level as the negative control (Fig. 6A). UL86 promoter driven

10   luciferase activity responded in a similar manner (Fig. 6A). When the same plasmid was tested in transient transfection assays in human HFF cells, the UL54 promoter was, as expected, specifically responsive to HCMV infection. Thus, transient expression from isolated HCMV promoters is apparently not specifically responsive to HCMV infection in murine cells.

To test if the non-responsiveness of the HCMV promoters was due to the nature of the

15   transient assay or to the inherent non-responsiveness of the HCMV promoters in murine cells, we generated neomycin resistant stable clones using the same plasmids. A total of 12 neomycin resistant UL54 promoter clones were isolated, four out of which showed some luciferase activity when infected with HCMV. The results for three representative clones are shown in Figure 6B (2A clones); the luciferase activity values were variable, ranging from 3 to 10-fold

20   peak activation at 24 hours post infection, decreasing by 48 hours postinfection. The non-infected samples had some residual activity in the absence of infection, most likely influenced by the site of integration. In order to examine whether the effect of HCMV infection is specific to the expression from UL86 (late promoter), stable cell lines containing the pLHN.UL86 plasmid were investigated. Since HCMV is unable to replicate in murine cells it was expected

25   that the UL86 promoter would not be activated if regulation is specific, while a non-specific enhancement would cause some expression upon infection. In these experiments the UL86

neomycin resistant clones (6A clones in Figure 6B) showed no significant activation of transcription either in the absence or presence of HCMV. Overall, the UL54 promoter, when isolated from its natural surrounding sequences, is poorly activated by HCMV infection in murine cells.

5   **Cloning and Mutagenesis of a HCMV Yeast Artificial Chromosome**

It is possible that the lack of a robust activation of UL54 may be due to integration in host chromatin and/or perhaps the lack of its natural sequence context. To investigate the influence of *cis*-acting sequences on the activity of the UL54 promoter in the context of its natural genomic location, a YAC was constructed with a 178 kb HCMV DNA fragment,

10   encompassing most of the UL (unique long) region of the viral genome (Figure 7; Y24). This part of the HCMV genome lacks the major immediate-early (IE) gene region, and is expected to be defective for viral growth. Briefly, the centromeric plasmid, pRML1+I$_2$, contains a 4895 bp DNA fragment from the 5' end of HCMV genome. The non-centromeric plasmid, pRML2(ura)+Ea, has a 3292 bp fragment from the 3' end of the UL region. Both plasmids

15   were co-transformed into the yeast strain YPH857 with HCMV DNA (strain Towne). Different clones were obtained, and the integrity of the selected YAC (Y24) was verified by several methods. If recombination between the two plasmids and the viral DNA is as expected, a new chromosome of around 178 kb should be generated, encompassing the HCMV genome from the 5' end to position 178816.

20   For the separation of yeast chromosomes a Biometra Rotaphor R 23 was used. The yeast DNA samples, agarose gels, and electrophoresis conditions were done following the directions provided by the manufacturer. To separate Y24, an artificial chromosome of approximately 180 kb, a 20 hour run was done at 180 volts, with 15 seconds intervals and a rotation angle of 120°.

25   Figure 8A (left panel) shows a PFGE of Y24, along with the parental strain YPH857. Y24 migrates as an approximately 180 kb extra chromosome in the stained gel. When the

separated chromosomes were hybridized to a HCMV UL54 specific probe, only Y24 showed

specific hybridization (Figure 8A, second panel).

To further test the overall integrity of the viral DNA, a sequence tagged site (STS)

analysis was performed with specific primer sets along the HCMV genome. DNA was

5   prepared from a yeast strain harboring Y24, and PCR was performed using 6 different pairs of

STS oligos specific to consecutive regions of HCMV (the locations of the STS are shown in

Figure 7).

For the STS, analysis specific pairs of primers were designed along the HCMV

sequence, with an approximate spacing between them of 20 kilobases, to be able to check for

10   intactness of the viral genome. A subset of those STS pairs was used in this study, as shown in

Figure 6. PCR was performed using either yeast total DNA of a strain containing Y24 or DNA

extracted from HCMV AD169 DNA as positive controls. Each PCR reaction contained 100 ng

of template DNA, and 25 pmol of each oligonucleotide of the STS pair in a total volume of 25

µl, using standard PCR conditions. The reactions were incubated one cycle at 94°C for 3

15   minutes, followed by 30 cycles of amplification of 30 seconds at 94°C, 1 minute at 50°C, and 1

minute at 72°C. An aliquot of the reaction was loaded in a 1% agarose gel, to check for the

presence of the expected DNA fragment size. The pair S22 (oligonucleotides S225,

ATGAGGATCGCGACAG (SEQ ID NO:52), and S223, CGTTATCCGTTCCTCG (SEQ ID

NO:53), positions 3809 and 4186 in the HCMV genome respectively) amplifies a DNA

20   fragment of 378 bp; the pair S04 (oligonucleotides S045, AGATGGATTCGTGCAC (SEQ ID

NO:54), and S043, ATCGATCTGGAGCACT (SEQ ID NO:55), positions 36489 and 36714

respectively) amplifies a DNA fragment of 226 bp; the pair S06 (oligonucleotides S065,

GGTCCGCAACTTCTGATCCA   (SEQ   ID   NO:56)   and   S063,

CAGATCAGTCCACAGGTTCT (SEQ ID NO:57), positions 66701 and 67183 respectively)

25   amplifies   a   fragment   of   483   bp;   the   pair   S08   (oligonucleotides   S085,

ACGCAGGTGAATATCC (SEQ ID NO:58), and S083, AGGTTATCGTCAAGCG (SEQ ID

31

NO:59), positions 84721 and 85094 respectively) amplifies a DNA fragment of 374 bp; the pair

S10 (oligonucleotides S105, GATGGTGGAAATCGGA (SEQ ID NO:60), and S103,

ATATCGCACCGATTGC (SEQ ID NO:61), positions 128975 and 129337 respectively)

amplifies a DNA fragment of 363 bp; the pair S12 (oligonucleotides S125,

GTTGGCGTTGAGCACGTCTA (SEQ ID NO:62), and S123,

AGCCGACAACCTGCTGCACT, (SEQ ID NO:63) positions 149371 and 149770 respectively)

amplifies a DNA fragment of 400 bp.

The results from the experiment are shown in Figure 8B, in which all the specific primer

sets amplified DNA fragments of the expected sizes, when compared to the viral DNA. This

result demonstrates the overall integrity of the 178816 bp of viral sequence.

The YAC was retrofitted for selection in mammalian cells so that the HCMV YAC

could be used for the analysis of essential *cis* acting sequences in a transgenesis system. The

first mutagenesis was targeted to the right arm of the YAC, to introduce the puromycin

resistance gene, a mammalian selectable marker. The *URA3* gene was substituted by *LEU2*

plus the puromycin resistance gene, using the plasmid pRML2-Leu2-PUR digested with *Not* I

(see Figure 7). This replacement is expected to provide a YAC with the same basic features on

the non-centromeric arm, but which now includes the mammalian selectable marker puromycin.

Recombinant yeast clones were selected in the corresponding medium (yeast synthetic medium,

SD, lacking tryptophan and leucine), and analyzed by PFGE and Southern blot analysis. The

expected 180 kb specific band appears in the stained PFGE gel and when the puromycin

resistance gene was used as a probe in a Southern blot analysis, only the newly made Y24P

YAC gave a specific signal of around 180kb, indicating that the integration had successfully

occurred (Figure 8A, right panel).

To investigate *cis*-acting sequences and their activity on the UL54 promoter in the

context of the UL region, a YAC, Y24P/UL54wt-Luc was constructed, in which a luciferase

reporter gene was inserted at position +20 of the UL54 promoter (Figure 7). The strategy was

as follows: SmaI–digested pLHN.UL54wt DNA, which contains the *HIS3* gene for selection in yeast, was retrofitted into a strain containing Y24P. The integration of the plasmid in the YAC sequence would produce histidine prototrophs, in which the correct integration can then be tested by PCR. Using specific primers, directed to the region adjacent to the UL54 promoter

5   but not included in the pLHN.UL54wt plasmid, and to the luciferase gene, a specific DNA fragment of the expected size (1.1 kb) was amplified (Figure 8C, lane 2, compare to Y24P, lane 1). This new YAC has, besides the UL54 promoter fused to luciferase and integrated in its natural position in the HCMV genome, the neomycin resistance gene, which confers an additional marker for positive selection in mammalian cells (see Figure 7).

10   In addition, in order to have a control for HCMV late gene expression, another YAC was constructed in which the luciferase gene was inserted downstream of the UL86 promoter. The strategy was very similar to the one used to generate the UL54-luciferase fusion, but in this case the plasmid pLHN.UL86 was retrofitted, digested with SmaI, in a yeast strain harboring Y24P (Figure 7). The recombinant clones were selected on medium lacking histidine, and as

15   previously described, the correct integration was confirmed by PCR, using specific primers directed to the region neighboring the UL86 promoter and the luciferase gene (Figure 8C, compare lanes 4 and 5).

Analysis of UL54 promoter activity by stable transfer (transgenesis) of HCMV-YAC to NIH 3T3 cells

20   Next, the influence of the surrounding UL region on UL54 transcription activity by direct transfer of Y24P/UL54wt-Luc into NIH 3T3 fibroblasts was examined. In these experiments, 10^8 yeast spheroplasts were fused to 2×10^6 mouse fibroblasts. Polyethylene glycol (PEG) spheroplast fusion was performed as described by Julicher *et al.* *Genomics*, 43:95-98 (1997). A yeast strain containing the YAC plasmid of interest was grown until it reached log

25   phase (OD_{600} 0.6-0.8). The cells were washed twice with water, and resuspended in SCE (1M Sorbitol, 0.1M Sodium Citrate, 60 mM EDTA, pH7.0), 9 mM DTT and 100 U/ml lyticase.

When the protoplasts were formed, they were washed twice with SCE. 10^8 yeast spheroplasts were fused to 2×10^6 NIH 3T3 cells in 0.5 ml 50%PEG 1500, 10 mM $CaCl_2$ for 2 minutes, then washed with serum-free medium and plated. After 48 hours, neomycin was added at a concentration of 400 µg/ml. Colonies appeared two weeks after applying the selection and resistant clones were isolated.

A total of 9 neomycin resistant clones were selected and first tested for luciferase activity after infection with HCMV at a M.O.I. of 10. Six of these clones showed some activity in the luciferase assays; three are shown in Figure 9 (clones 31C, 42.8 and 44.11). UV inactivated virus failed to elicit a response and the response of the UL54 promoter to infection in the YAC transgenic lines is proportional to the multiplicity of infection (Figure 10). To check the integrity of transferred YACs we performed a STS analysis, using some of the specific pairs of oligos along the HCMV genome. As shown in Figure 11, PCR reactions using DNA extracted from NIH 3T3 did not amplify any DNA fragment of the expected size. However, DNA from both the yeast strain Y24P and from the transgenesis YAC clones showed amplified DNA fragments of the expected size, indicating that intact YACs had been successfully transferred to NIH 3T3 cells (Figure 11). In marked contrast to the plasmid transgenic lines, as shown in Figure 9A, the YAC containing NIH 3T3 cells showed very low luciferase activity when mock-infected; 24 hours post infection with HCMV they exhibited a very strong up regulation, which continued to increase up to 48 hours (Figure 9A). Furthermore, the absolute values of luciferase activity in the stable YAC clones were less variable and consistently higher than the stable plasmid-containing cell lines. The basal reporter gene levels in mock-infected YAC transgenic cells are subject to a highly specific and very tight regulation.

A comparison between the plasmid and the transgenesis cell lines showed a very strong activation of the UL54 promoter upon HCMV infection ranging from 170 at 24 hours to 470-fold at 48 hours post infection in the YAC cell lines (Figure 9B). This activation is very high

compared to the stable plasmid clones, suggesting positive influence of remote viral DNA sequences in addition to more stringent regulation prior to activation. It is noteworthy that the second peak of activation at 48hrs is not observed with the plasmid transgenic lines.

Transgenesis experiments were also carried out with the Y24P/UL86 to murine cells. 5   The UL86 promoter is a true L promoter (Chambers *et al. J. Virol.* 73:5757-66 (1999), which is activated only after the onset of DNA replication. The transfer yielded three neomycin resistant clones, and the presence of the YAC sequences was tested by Southern blot and STS analysis . None of these clones showed any luciferase activity before or after infection with HCMV (Figure 9A, clones 5C and 7E). The lack of activation of UL86 transcription in the transgenesis 10   experiments indicates the expected restriction in replication of HCMV in murine cells. Altogether, these results underscore the importance of sequence context in providing optimal level of gene expression.

Analysis of the UL54 promoter activation pathway by HCMV in murine cells

The primary pathway for early activation of the UL54 promoter is dependent on IE86 15   mediated activation via the IR1 element that binds the cellular transcription factor Sp1. In order to investigate the early activation pathway of HCMV UL54 in murine cells, we accordingly mutated the IR1 element present in the UL54 promoter. Kerry *et al. J. Virol.* 70:373-82 (1996). Figure 7 shows the point mutations introduced in the IR1 site, which has been previously shown to completely eliminate IE86 transactivation of the UL54 promoter. Kerry *et al. J. Virol.* 20   68:4167-76 (1994).

In agreement with previous studies, the mutant plasmid (pLHN.UL54IRM) showed a much lower activation after transfection in HFF human cells and infection with HCMV (around 17-fold reduction), when compared to the wild type counterpart. Kerry *et al. J. Virol.* 70:373-82 (1996). On the basis of this result the plasmid pLHN.UL54IRM was retrofitted into Y24P, 25   to study the effect of the IRM mutation in the UL54 promoter, in the context of the UL region. Figure 7 shows a schematic of the recombinant generated in yeast (Y24P/UL54IRM-Luc) and

its integrity was confirmed by PFGE, STS analysis and Southern blot hybridization. Transgenesis studies were performed next by spheroplast fusion of the Y24P/UL54IRM-Luc to NIH 3T3. The PEG fusion produced 8 neomycin resistant clones, three of which showed luciferase activity after infection with HCMV (Figure 12). The profile of activation, with a

5   peak at 24 hours, was different to the UL54 wild type promoter (compare Figures 9B and 12), but most significantly, both the absolute values and the extent of the activation (10 to 30-fold, Figure 12), were significantly diminished. The remaining activity is most likely due to the ATF binding site positioned upstream of the IR-Sp1 element of the UL54 promoter. See Kerry et al., J. Virol. 70:373 (1996). These results suggest that the pathway used for HCMV early activation

10   of the UL54 promoter is conserved in murine cells, and that the same or functionally similar cellular factors bind to the UL54 promoter. In agreement with this view, we observe IE1 and UL54 RNA upon infection with HCMV (Figure 14).

Figure 14 shows the detection of HCMV IE1 and UL54 transcripts in 3T3 cells infected with HCMV. NIH 3T3 or HFF cells were mock infected (M) or infected with HCMV at an

15   MOI of 1. Total RNA was harvested at different times (hour postinfection) indicated, treated with DNase, and reverse transcribed by using oligo(dT). PCRs were performed using primer sets specific for HCMV IE1 UL54, human TF (for HFF samples), and murine HPRT (for NIH 3T3 samples).

Briefly, NIH 3T3 or HFF cells were infected with the Towne strain of HCMV at a

20   M.O.I. of 1. Total RNA was isolated at different times after infection by the RNAzol method (Tel-Test, Inc. Friendswood, TX) according to the manufacturer's protocol. RNA samples were treated with RNase-free DNase I for 15 min. at room temperature, and the DNase was inactivated at 65°C for 15 min. The RNA was reverse transcribed using oligo(dT) primers at 42° for 50 min., and reactions were terminated by heating at 70°C for 15 min. The reverse-

25   transcribed products were treated with RNaseH for 20 min. at 37°C and amplified using specific primers. Primers IEP4BII (CAATACACTTCATCTCCTCGAAAGG; SEQ ID NO:65) and

IEP3C (CAACGAGAACCCCGAGAAAGATGTC; SEQ ID NO:66) were used to amplify a

217-bp product within the HCMV *ie1* gene (see Kondo et al. Proc. Nat. Acad. Sci. USA,

91:11879 (1994)), and primers RTUL54-2R (AAGCCGGCTCCAAGTGCAAGCGCC; SEQ

ID NO:67) and RTUL54-6F (CGTGTGCAACTACGAGGTAGCCGA; SEQ ID NO:68) were

5   used to amplify a 199-bp fragment within the HCMV UL54 gene. Primers TF-R and TF-F,

designed to amplify a 601-bp product within the human tissue factor (TF) gene, and primers

HPRT-R and HPRT-F, designed to amplify a 163-bp within the murine hypoxanthine

phosphoribosyltransferase (HPRT) gene, have been previously described (Angulo et al. J.

Virol., 72:2826 (2000); Kurz et al. J. Virol. 71:2980 (1994)). PCRs were performed under the

10   following conditions: 1 cycle at 94°C for 3 min.; 30 cycles of 1 min. at 94°C; 1 min. at 60°C;

and 1 min. at 72°C; and 1 cycle at 72°C for 10 min. Control reactions carried out in the absence

of reverse transcriptase were used to assess the specific detection of RNA. Amplified products

were separated on 1% agarose gel and visualized by ethidium bromide staining. Sizes were as

expected for each primer set. Specific PCR-amplified products were not detected in control

15   reactions in which reverse transcriptase was not added during the RNA reverse transcription

reaction. From these experiments we conclude that HCMV E activation of the UL54 promoter

by IE transactivators is not restricted by host species encoded cellular factors.

**Analysis of the MCMV activation of the HCMV UL54 promoter in YAC
transgenic clones**

20   In the experiments described above, a homologous promoter-virus relationship was

maintained in a heterologous host cell background, and the pathway of activation of E gene

expression uses the same cellular pathway in both human and murine cells was demonstrated.

Knowing that the cellular pathway is conserved between human and murine cells, the effect of

changing the species origin of the virus was next tested. For these experiments the YAC

25   transgenic clones Y24P/UL54wt-Luc 31C and 44.11 were infected with MCMV, and their

levels of activation of the UL54 promoter were examined. In this scenario the cell-virus

relationship is homologous (both are murine), while the promoter-virus relationship is heterologous.

Two of the Y24P/UL54wt-Luc stable clones were infected with MCMV, at an M.O.I. of 10, and the luciferase activity at 24 and 48 hours post infection was analyzed. The maximum transcriptional activity was ten-fold lower in the MCMV infection, in comparison with the activation by HCMV (Figure 9B and 13, clones 31C and 44.11). This lower activation points towards a restriction at a viral *trans*-acting factor level, making necessary the concordance of species origin of both promoter and viral *trans*-activators to recapitulate the activation profile of the UL54 promoter. As anticipated, the Y24P/UL86-Luc 5C and 7C clones were not activated by MCMV infection (Figure 13). Taken together, these results suggest that there is a dominance of virus over host factors in determining species specificity of E gene expression.

In this Example a YAC transgenesis approach was used to examine the species restriction checkpoint of an essential early gene activation pathway of HCMV in murine cells. Toward this end a YAC vector was designed, encompassing most of the UL region of HCMV. This vector is replication defective, lacks the major IE region, thus permitting the analysis of essential *cis*-acting sequences within the UL region when complemented in *trans*. For the purpose of this study we chose to study essential *cis*-acting sequences of the viral DNA polymerase (UL54) promoter complemented by HCMV infection in murine cells. The isolated UL54 promoter, both in transient and stable transfections, showed a profile of activation not in accordance with an early gene. Only when in the context of the UL region, the UL54 promoter was able to recapitulate the early (48 hr post infection) gene activation described in human cells. Kerry *et al. J. Virol.* 70:373-82 (1996). The same plasmids were used for the transfection assays and for the YAC mutagenesis, to avoid variability. In the UL54wt plasmid stable clones, the basal activity in mock-infected cells was not as tightly regulated as in the YAC clones, and the extent and profile of activation was more random. This suggests the need for tight regulation of early events, and perhaps the involvement of long-range *cis* acting sequences

(sequence context) for optimal UL54 gene regulation. Indeed, the results of this study strongly

support the suggestion that remote regulatory sequences participate in the control of expression

of this essential early gene.

Members of the CMV family have evolved by co-speciation with their host and as a

5   consequence have had sufficient time for acquiring a significant degree of genetic drift.

McGeoch et al., J. Mol. Biol. 247:443-58 (1995). In particular, the genetics of HCMV

speciation has lead to the non-viable replication in other host species. In this case we can

assume that genetic changes that have been beneficial or neutral to its natural host background

may well be deleterious to another host genetic background because of negative or

10   inappropriate gene interactions that had not been screened by natural selection. For this reason

species-specific strains of CMV must have accumulated genetic changes that may be

advantageous or neutral with its host species but that produce non-viability in different host

species. The results of this study suggest that the virus-host gene interaction pathway for E

gene activation is viable between different host species but has significantly diverged between

15   virus species. This strongly argues for co-evolution of viral transacting factors and their viral

target promoters. In agreement, the mutation of the IR1 element of the HCMV UL54 promoter

showed that the pathway of E activation is equivalent in human and murine cells. Thus, IE86

mediated activation of UL54 via the IR1 element is conserved in murine cells. In support, the

primary host factor known to bind the IR1 element is Sp1, in which sequence homology

20   between human and murine Sp1 is over 95%. In contrast, the MCMV transactivator (IE3) not

only exhibits more sequence differences (<40% identity) from its related HCMV (IE86)

counterpart but also is extremely inefficient at activating the HCMV UL54 promoter via the

IR1 element, indicating a divergence of mechanism of action. A prediction from these

observations is that it would not be informative to study HCMV IE proteins in the context of

25   MCMV infection. Consistent with this notion, we find that IE3 mutant of MCMV is poorly

complemented by HCMV infection in murine cells (AA & PG, unpublished results).

In summary, Example 4 shows the use of a YAC transgenesis system to explore critical host-viral gene interaction pathways in the cross species activation of a key early gene promoter of HCMV, UL54. Example 4 shows a clear dominance of virus factors (major immediate early

5   proteins) for the transactivation of the UL54 early promoter, and point for a species specificity checkpoint at later times of infection.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the

10   invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

All publications and patent applications mentioned in this specification are herein

15   incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

CLAIMS

We claim:

1.   An isolated recombinant DNA molecule comprising a yeast artificial chromosome including at least a portion of a human cytomegalovirus (HCMV) genome.

2.   The isolated recombinant DNA molecule of claim 1, the DNA molecule further comprising at least one *a* sequence.

3.   The isolated recombinant DNA molecule of claim 1, said HCMV genome being derived from a HCMV Towne strain.

4.   The isolated recombinant DNA molecule of claim 1, said HCMV genome being derived from a HCMV AD169 strain.

5.   The isolated recombinant DNA molecule of claim 1, wherein said DNA molecule comprises a DNA molecule selected from the group consisting of Y1-2, Y3-2, Y2-4, Y4-7 and Y5-26, as shown in Table 2 and SEQ ID NO:64.

6.   The isolated recombinant DNA molecule of claim 1, wherein said DNA molecule comprises clone Y5-26.

7.   The isolated recombinant DNA molecule of claim 1, wherein said recombinant DNA molecule is the recombinant DNA molecule contained in ATCC deposit chosen from the group consisting of ATCC No. PTA-2186 and ATCC No. PTA-2187.

8.   A composition suitable for use as a vaccine comprising the isolated recombinant DNA molecule of claim 1 and a pharmaceutically acceptable excipient.
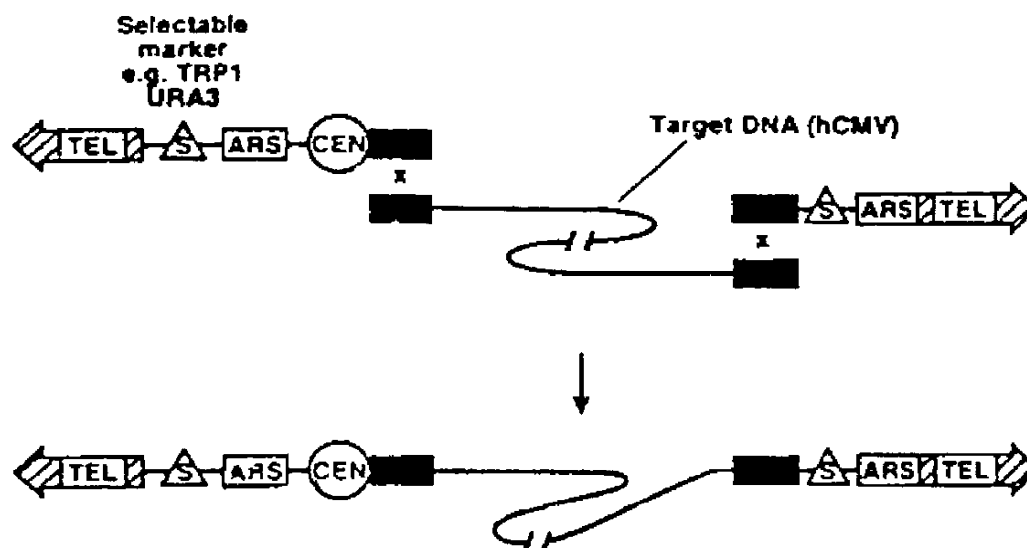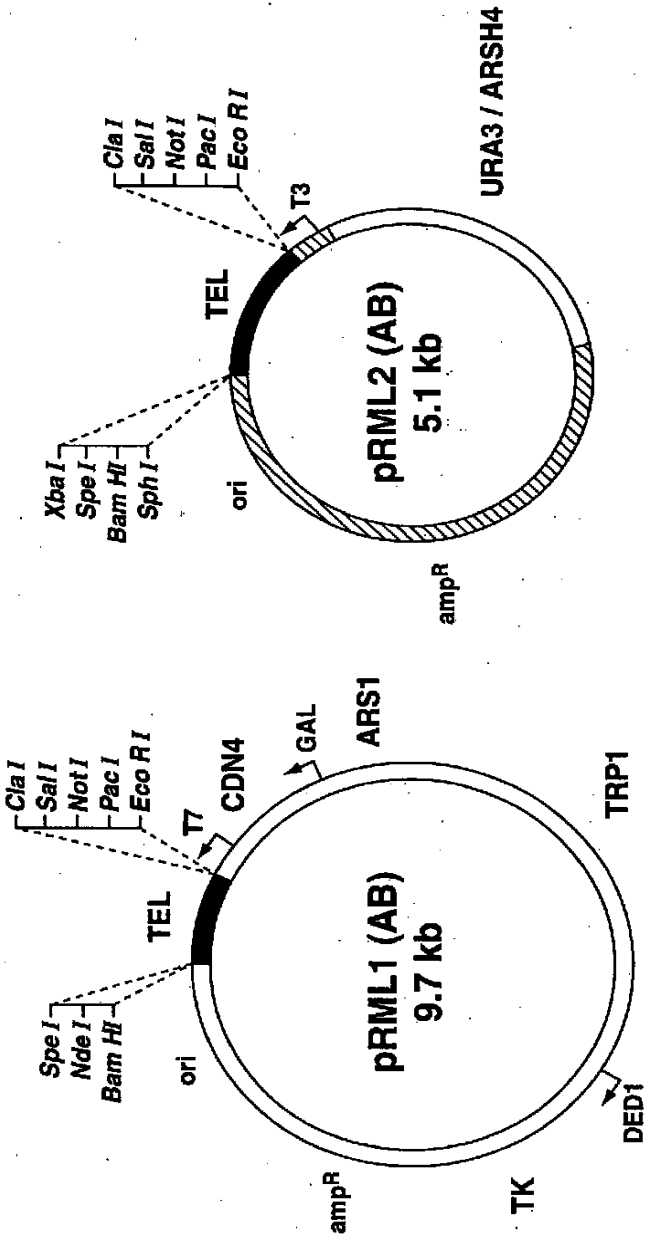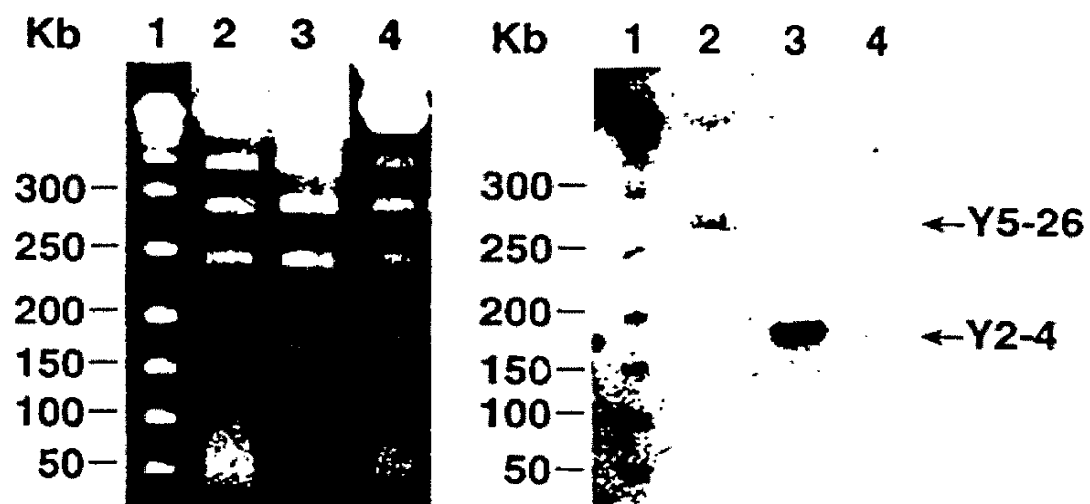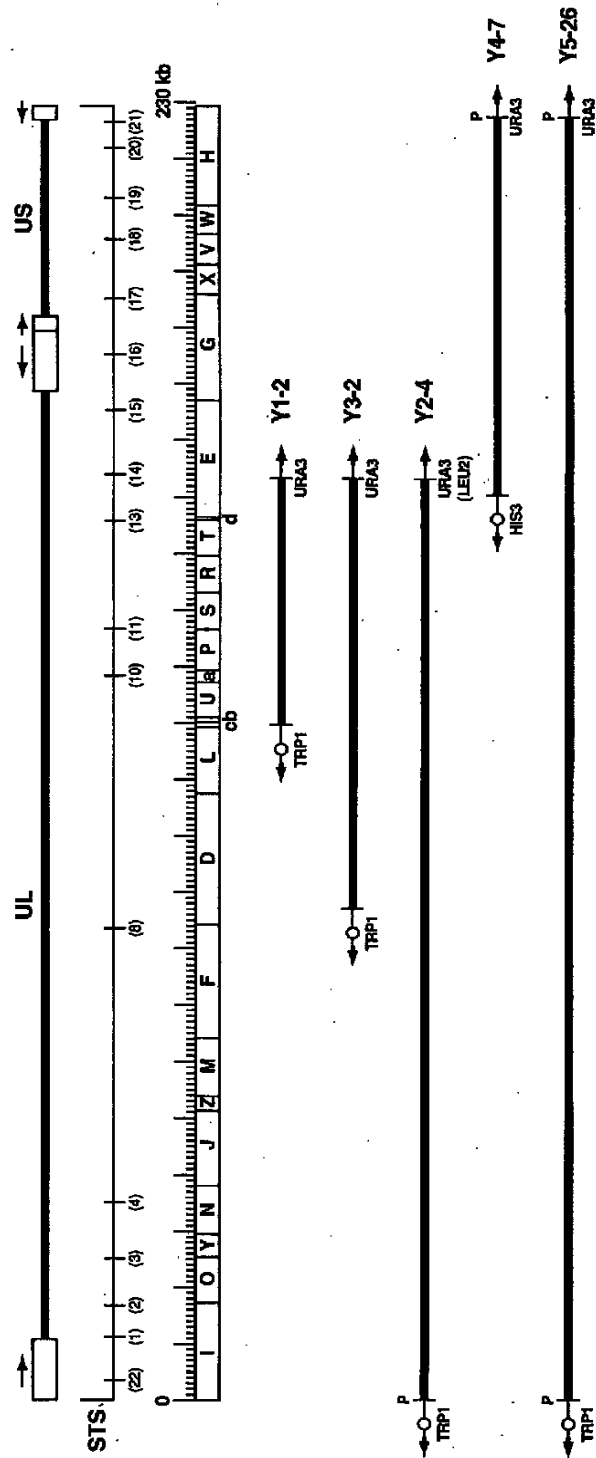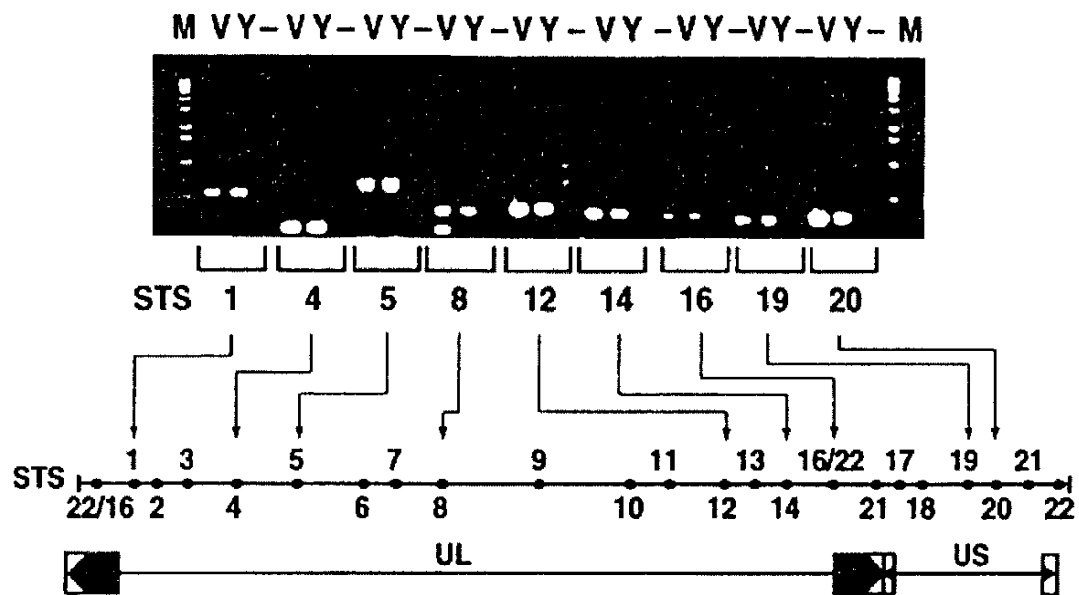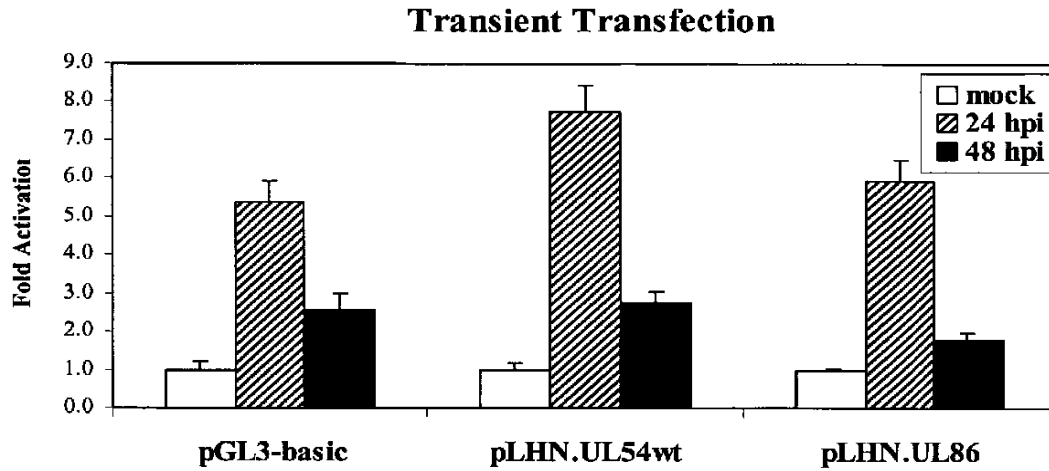
Fig. 1

Fig. 2

Fig. 3

4/12

Fig. 4

Fig. 5

Transient Transfection

Fig. 6A

Stable Transfection

Fig. 6B

7/12
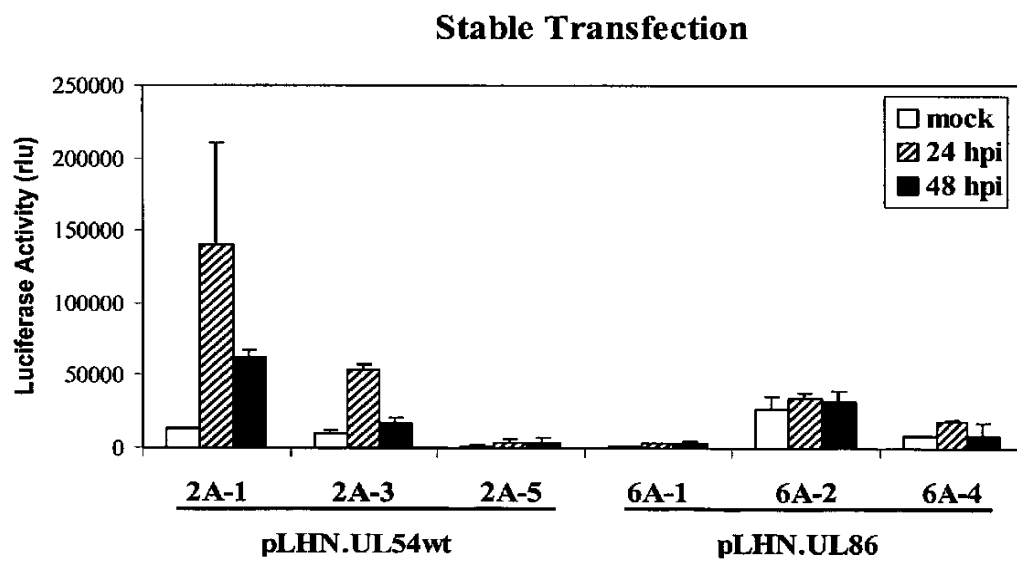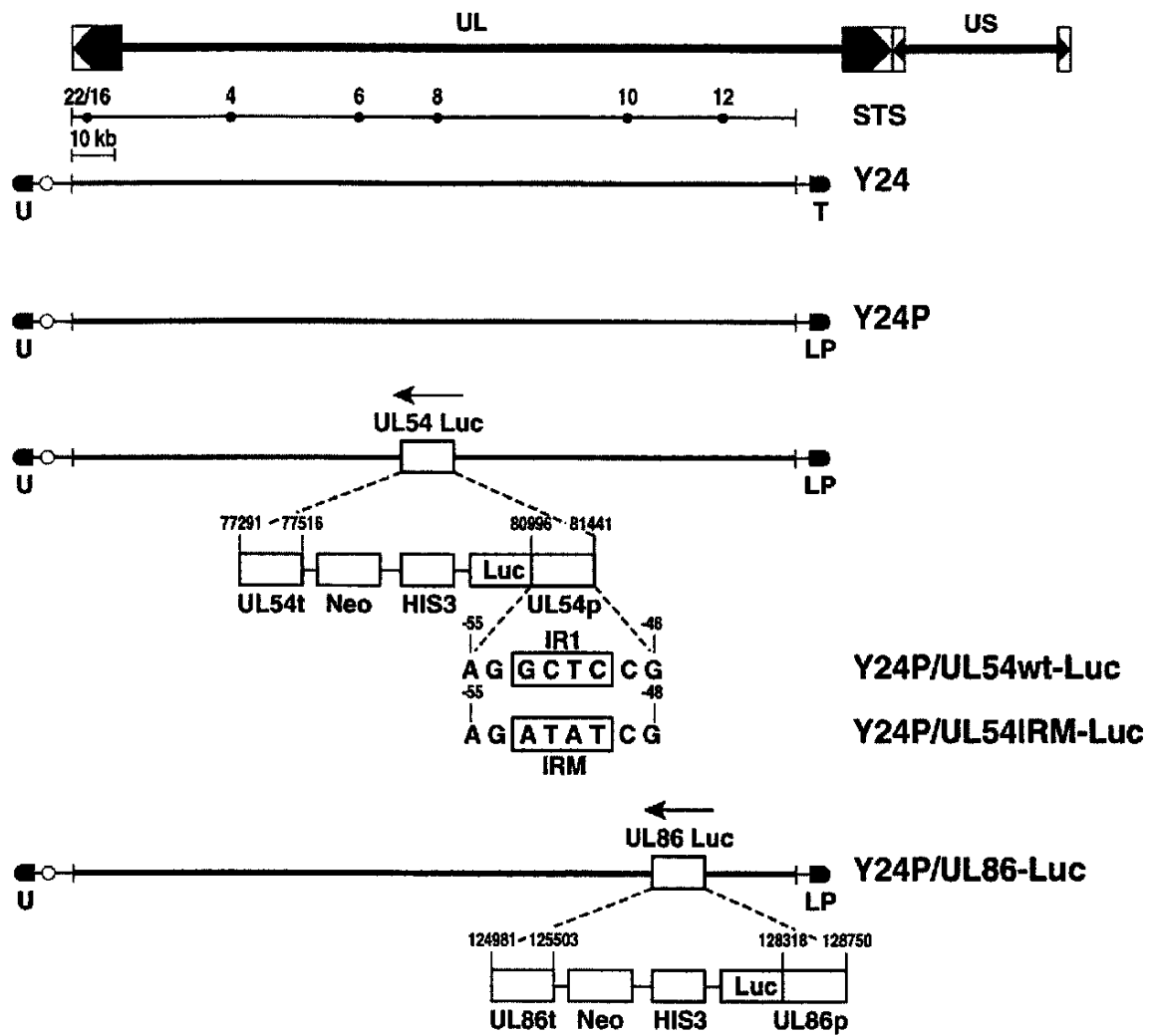
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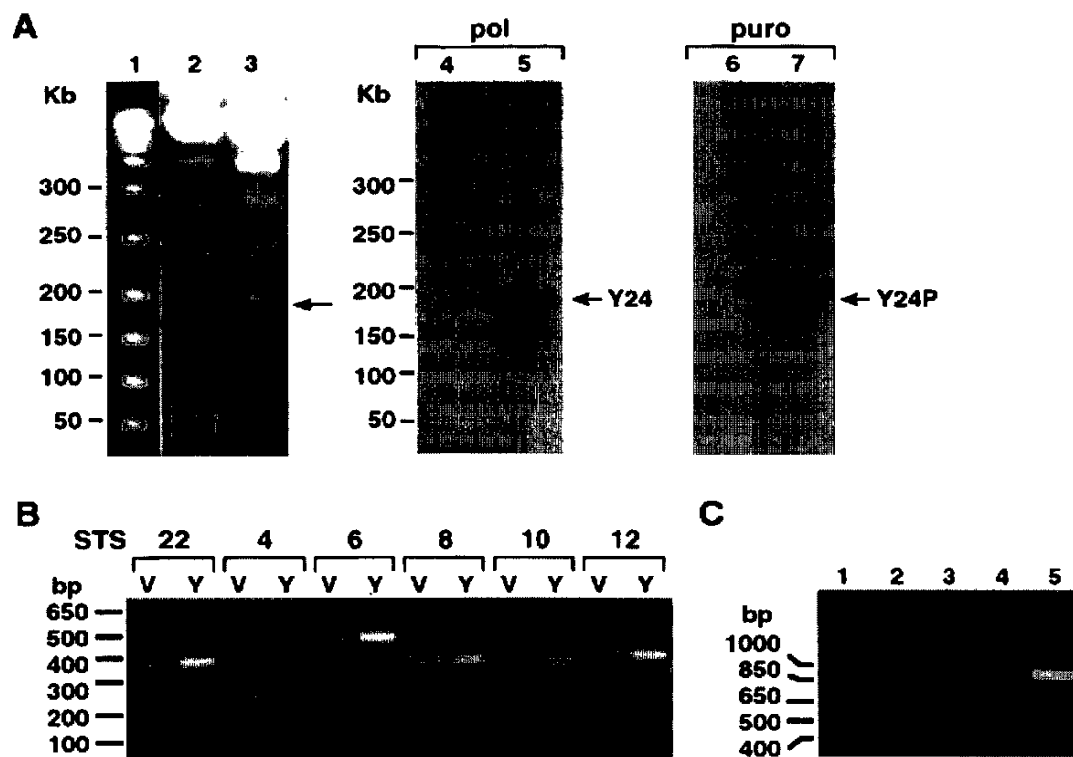
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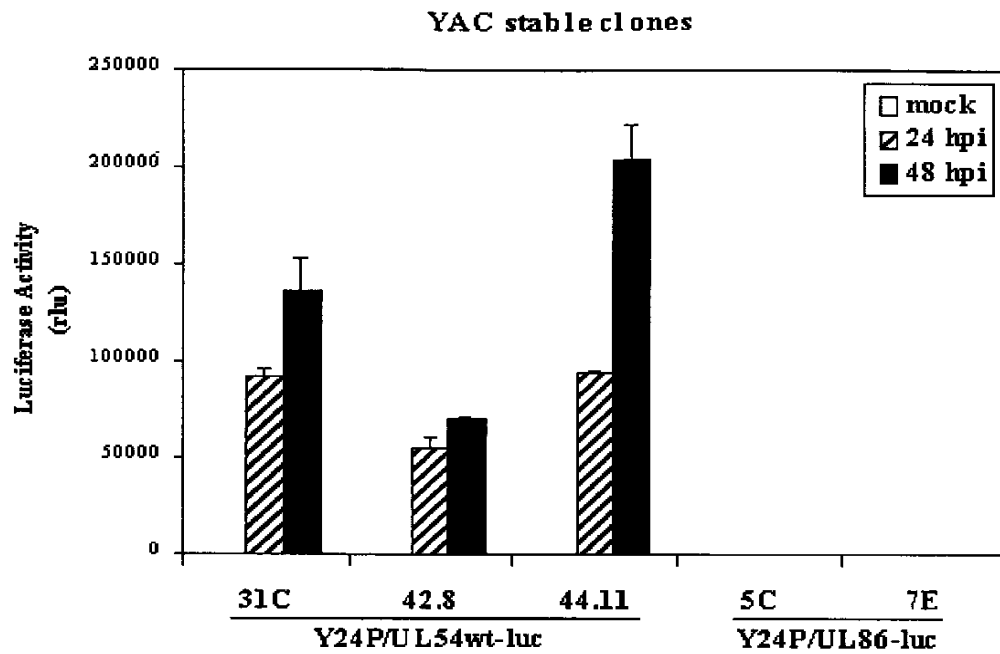
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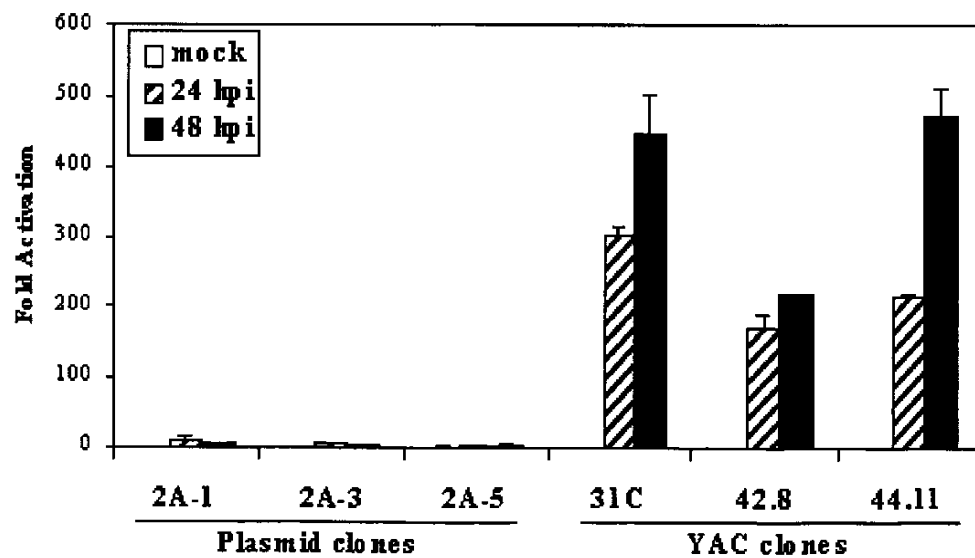
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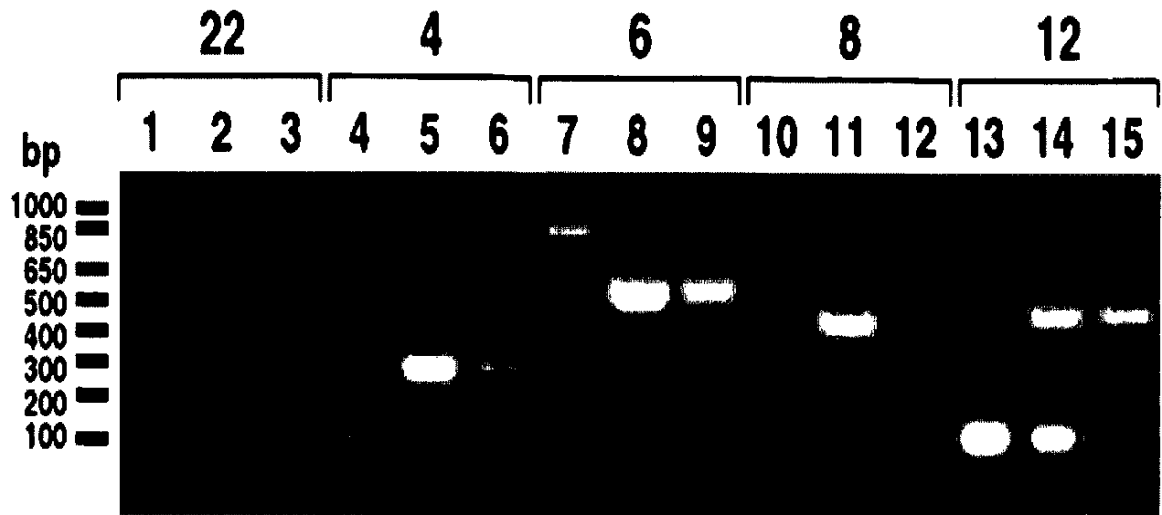
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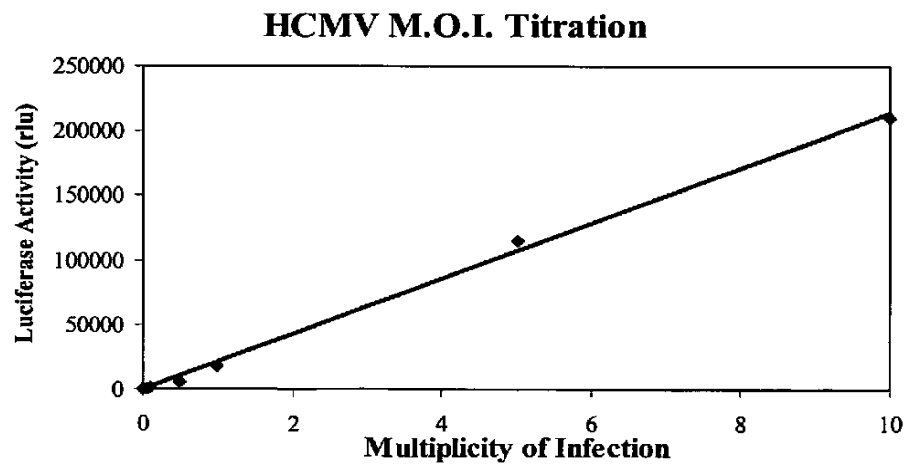
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Y24p/UL54IRM-luc Stable Clones
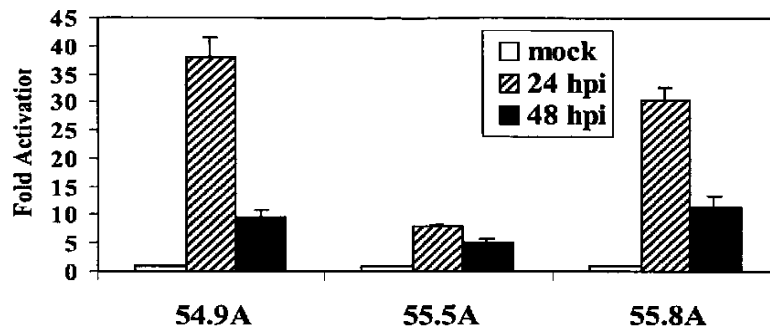
Fig. 12

MCMV Infection of YAC Clones
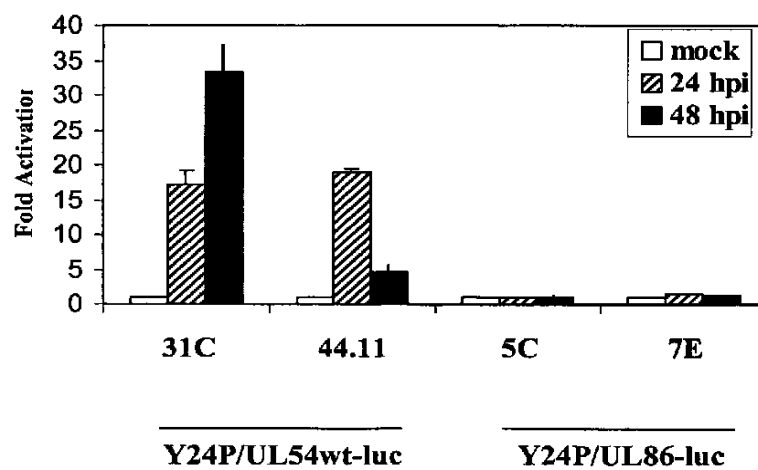
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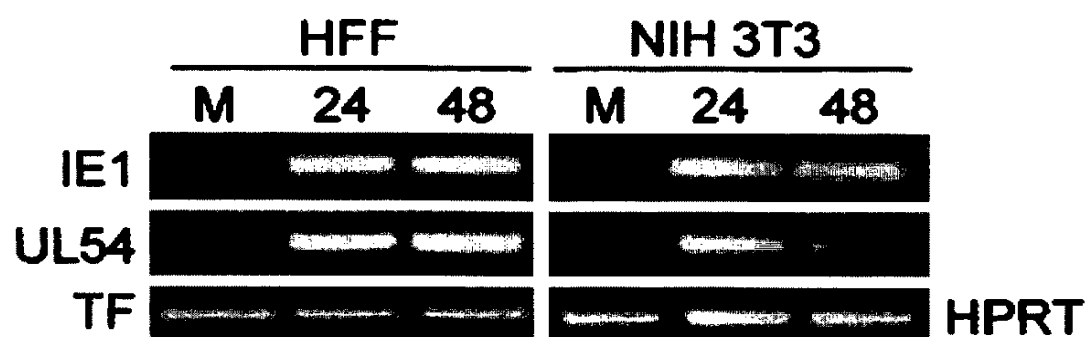
Fig. 14

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<120> Generation of Human Cytomegalovirus Yeast Artificial Chromosome
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